



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 162745**

**TO: Pablo Whaley**  
**Location: rem/4C35/2C70**  
**Art Unit: 1631**  
**Friday, March 24, 2006**  
**Case Serial Number: 10/509595**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**  
  
**toby.port@uspto.gov**

### **Search Notes**

**Examiner Whaley,**

**See attached results.**

**If you have any questions about this search feel free to contact me at any time.**

**Thank you for using STIC search services!**

**Toby Port**  
**X22523**

**This Page Blank (uspto)**

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 01:14:39 ; Search time 28911 Seconds  
(without alignments)  
11796.918 Million cell updates/sec

Title: SEQ1-4037A

Perfect score: 6000  
Sequence: 1 gctccacaggaagctctccccc.....atcagggagactcatgtac 6000

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sra:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5998.4	99.9	79376	8 HS454G6	Z98750 Human DNA s
2	5972	99.5	170425	14 AC0024490	AC0024490 Homo sapi
3	4888.8	81.5	6169	6 AR123665	AR123665 Sequence
4	4888.8	81.5	6169	6 BD065041	BD065041 Methods f
5	4888.8	81.5	6169	6 BD237936	BD237936 Nucleic a
6	4888.8	81.5	6169	6 AR242746	AR242746 Sequence
7	4069.4	67.8	5300	6 AR123663	AR123663 Sequence
8	4069.4	67.8	5300	6 BD237934	BD237934 Nucleic a
9	4069.4	67.8	5300	6 AR242744	AR242744 Sequence
10	4068.4	67.8	5299	6 BD065039	BD065039 Methods f
11	4057.4	67.6	5304	6 AR123664	AR123664 Sequence
12	4057.4	67.6	5304	6 BD065040	BD065040 Methods f
13	4057.4	67.6	5304	6 BD237935	BD237935 Nucleic a
14	4057.4	67.6	5304	6 AR242745	AR242745 Sequence
15	4044.8	67.4	5300	8 AF007562	AF007562 Homo sapi
16	4015.8	66.9	5271	6 BD237961	BD237961 Nucleic a
17	4015.8	66.9	5271	6 AR242771	AR242771 Sequence
18	2773.4	46.2	2800	6 BD225246	BD225246 Remedies

19	2773.4	46.2	2800	6 AR212944	AR212944 Sequence
20	2773.4	46.2	2800	6 AR532546	AR532546 Sequence
21	2773.4	46.2	2800	8 HSMYOC1	AF049791 Homo sapi
22	1225.2	20.4	3163	8 AB006688	AB006688 Homo sapi
23	1068.8	17.8	1086	8 HSGLC1A1	Z97171 Homo sapien
24	1043.8	17.4	1311	8 AY190128S1	AY190128 Macaca fa
25	770	12.8	2166	6 AR163697	AR163697 Sequence
26	770	12.8	2166	6 BD009308	BD009308 Gilaucoma-
27	677.8	11.3	2145	6 AX300008	AX300008 Sequence
28	664.4	11.1	2111	8 BC029261	BC029261 Homo sapi
29	651.2	10.9	1934	8 D88214	D88214 Homo sapien
30	640.4	10.7	1548	6 AR123688	AR123688 Sequence
31	640.4	10.7	1548	6 BD065064	BD065064 Methods f
32	640.4	10.7	1548	6 BD237959	BD237959 Nucleic a
33	640.4	10.7	1548	6 AR242769	AR242769 Sequence
34	640.4	10.7	1871	6 AX004457	AX004457 Sequence
35	640.4	10.7	1871	6 AX004474	AX004474 Sequence
36	640.4	10.7	1999	6 AR030962	AR030962 Sequence
37	640.4	10.7	1999	6 AR066022	AR066022 Sequence
38	640.4	10.7	1999	6 AR069089	AR069089 Sequence
39	640.4	10.7	2000	8 HSU85257	U85257 Human trade
40	640.4	10.7	2002	6 AB4847	AB4847 Sequence 2
41	635.6	10.6	2000	6 AB4850	AB4850 Sequence 2
42	626.4	10.4	2045	6 CQ726274	CQ726274 Sequence
43	626.4	10.4	2061	8 HSAF001620	AF001620 Homo sapi
44	626	10.4	23704	9 AF289236	AF289236 Mus muscu
45	626	10.4	188661	9 AC138218	AC138218 Mus muscu

#### ALIGNMENTS

RESULT 1  
HS454G6/c  
LOCUS  
DEFINITION  
Human DNA sequence from clone RP3-454G6 on chromosome 1q24 contains the 3' end of the gene for HBxAg transactivated protein 2 (XTP2) and the MYOC gene for myocilin, trabecular meshwork inducible glucocorticoid response, complete sequence.

ACCESSION  
Z98750  
VERSION  
Z98750.1 GI:2887277  
KEYWORDS  
HTG; glucocorticoid; HBxAg; MYOC; myocilin; transactivated protein 2; XTP2.

SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
1 (bases 1 to 79376)  
Pavitt R.  
Direct Submission  
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

TITLE  
JOURNAL  
COMMENT  
On Feb 14, 1998 this sequence version replaced gi:2465060.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
Embl, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMBEP; Information on the WORMBEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1  
RP3-454G6 is from the library RP3-3 constructed by the group of P. J. Pater de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pCVPAC2

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: vegas@sanger.ac.uk





polyA\_site 3971  
/gene="RP4-598F2.1"  
/locus\_tag="RP4-598F2.1-001"  
complement(45878..63132)  
/gene="MYOC"  
/locus\_tag="RP3-454G6.1-001"  
complement(join(45878..47170,49058..49183,62469..63132))  
/gene="MYOC"  
/locus\_tag="RP3-454G6.1-001"  
/product="myocilin, trabecular meshwork inducible glucocorticoid response"  
/note="match: cDNAB: Em:AF001620.1 Em:BC029261.1 Em:D88214.1 Em:U85257.1"  
complement(45878)  
/gene="MYOC"

polyA\_site

Query Match 99.9%; Score 5998.4; DB 8; Length 79376;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTCCACAGGAAGTCTCCCACTCTAGACTTGTGATCAGAGTTTACAGCCAGAAAGTTC 60  
DB 67191 GCTCCACAGGAAGTCTCCCACTCTAGACTTGTGATCAGAGTTTACAGCCAGAAAGTTC 67132

QY 61 CGTGAAGGTGAGGGGTCTGTGTCTTACACCTTATGCTTACACCTGAGCTCATGTC 120  
DB 67131 CGTGAAGGTGAGGGGTCTGTGTCTTACACCTTATGCTTACACCTGAGCTCATGTC 67072

QY 121 AACCTCTGCTCCCAAGTTCAGCAATTCTCTGTCTCAGCTCCGCGTACGCTGGAGT 180  
DB 67071 AACCTCTGCTCCCAAGTTCAGCAATTCTCTGTCTCAGCTCCGCGTACGCTGGAGT 67012

QY 181 ACAGGCGCAGCCCGGCTAATTTTGTATTTAGTAGAGTGGGGTTTCAACCATTTAG 240  
DB 67011 ACAGGCGCAGCCCGGCTAATTTTGTATTTAGTAGAGTGGGGTTTCAACCATTTAG 66952

QY 241 CCCGCTGTCTTGAATCTCTGACCTCAGGTGATCCACCACCTCAGCTCTTAAAGTGC 300  
DB 66951 CCCGCTGTCTTGAATCTCTGACCTCAGGTGATCCACCACCTCAGCTCTTAAAGTGC 66892

QY 301 TGGGATTAAGGATGATGATCCGCGCCCGGCGCAAGGGTCAGTGTTTAATAGAAATTAAC 360  
DB 66891 TGGGATTAAGGATGATGATCCGCGCCCGGCGCAAGGGTCAGTGTTTAATAGAAATTAAC 66832

QY 361 TTGAATGTTTACTAAACCAAGGGAACAGCAAAAGCTGATTAATTTACAGGATTC 420  
DB 66831 TTGAATGTTTACTAAACCAAGGGAACAGCAAAAGCTGATTAATTTACAGGATTC 66772

QY 421 TTGGGATGAGGAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGATCTTCATCA 480  
DB 66771 TTGGGATGAGGAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGATCTTCATCA 66712

QY 481 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTAACATTTTATTCACATGCTTTTGTG 540  
DB 66711 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTAACATTTTATTCACATGCTTTTGTG 66652

QY 541 GTAAGCTTCACATGTTTACTGAATTAAGATTAATCAATTAACATTAATTTGGGGCCA 600  
DB 66651 GTAAGCTTCACATGTTTACTGAATTAAGATTAATCAATTAACATTAATTTGGGGCCA 66592

QY 601 TCTGTGTGTGTATAGGGAGAGGAGGACATCCCGAGAGCTCTTTGAAGCCCGCGAG 660  
DB 66591 TCTGTGTGTGTATAGGGAGAGGAGGACATCCCGAGAGCTCTTTGAAGCCCGCGAG 66532

QY 661 AGGTTTCTCTCCAGCTGGGGAGGCTTGCAGAACCCCGGGGTCTGGGGTCTTGAAGCA 720  
DB 66531 AGGTTTCTCTCCAGCTGGGGAGGCTTGCAGAACCCCGGGGTCTGGGGTCTTGAAGCA 66472

QY 721 ACCCTGACAGCCCGTGCACCTGATGTTTGTATATCACTCTTAAGGAACTGTTGCTTCT 780  
DB 66471 ACCCTGACAGCCCGTGCACCTGATGTTTGTATATCACTCTTAAGGAACTGTTGCTTCT 66412

QY 781 ATTCTGTGTGACTGGTTCATTCATCCAGGCAATTCAGCAATTAATTAAGTACTTATA 840

DB 66411 ATTCTGTGTGACTGGTTCATTCATCCAGGCAATTCAGCAATTAATTAAGTACTTATA 66352

QY 841 TCTGCCAGACACCAAGACAAATAATGTGTAGCAAAAGCATCTGCTTCTGTGTAG 900  
DB 66351 TCTGCCAGACACCAAGACAAATAATGTGTAGCAAAAGCATCTGCTTCTGTGTAG 66292

QY 901 GTGACAGTTTCTCATAGGAAGGTGAGAAAGAAATTAATACCGCCAACTTAACCCA 960  
DB 66291 GTGACAGTTTCTCATAGGAAGGTGAGAAAGAAATTAATACCGCCAACTTAACCCA 66232

QY 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAACA 1020  
DB 66231 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAACA 66172

QY 1021 GGCACCTCTCCTAGCGCCCTCTGCTCATCTGTGCCCGAGGCCCCCAAGCCGAGT 1080  
DB 66171 GGCACCTCTCCTAGCGCCCTCTGCTCATCTGTGCCCGAGGCCCCCAAGCCGAGT 66112

QY 1081 CTTCCAGCTCTCCTCATGATGTCAGCGGCTGAGCTGAGCTTCCGTTCCCGTG 1140  
DB 66111 CTTCCAGCTCTCCTCATGATGTCAGCGGCTGAGCTGAGCTTCCGTTCCCGTG 66052

QY 1141 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGTGGCTCAGGCTCCAGAAAGAAATG 1200  
DB 66051 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGTGGCTCAGGCTCCAGAAAGAAATG 65992

QY 1201 AAGGGAATCTAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTTCCTCAGAGGAAG 1260  
DB 65991 AAGGGAATCTAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTTCCTCAGAGGAAG 65932

QY 1261 GCCTCAGCTCCAGAGAAATTCAGAGGTGGGACTGAGGAATGGGGAAGCTGGGCT 1320  
DB 65931 GCCTCAGCTCCAGAGAAATTCAGAGGTGGGACTGAGGAATGGGGAAGCTGGGCT 65872

QY 1321 TGAGCGGGTGTGAAAGCAAGGAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 1380  
DB 65871 TGAGCGGGTGTGAAAGCAAGGAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 65812

QY 1381 AGTGTGTTCACGAGGAGTGGAGATTTCCGTTGCTCTGTGAGGCTTTTATCTTTTCT 1440  
DB 65811 AGTGTGTTCACGAGGAGTGGAGATTTCCGTTGCTCTGTGAGGCTTTTATCTTTTCT 65752

QY 1441 CTGCTTGAAGGAAGAAAGTCTAATTCATGAAGGATGCAAGTTTATAAGTCACTGTT 1500  
DB 65751 CTGCTTGAAGGAAGAAAGTCTAATTCATGAAGGATGCAAGTTTATAAGTCACTGTT 65692

QY 1501 AAAATTCAGAGGTGATGAGGATTTCCCTTACAGAAAGCCTTATTAATGGAATATAG 1560  
DB 65691 AAAATTCAGAGGTGATGAGGATTTCCCTTACAGAAAGCCTTATTAATGGAATATAG 65632

QY 1561 GAAGGAGCTAATTCCTAGGCGGTTAATTCACGGAAGTACTGAGTCTTTCTTT 1620  
DB 65631 GAAGGAGCTAATTCCTAGGCGGTTAATTCACGGAAGTACTGAGTCTTTCTTT 65572

QY 1621 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGAGACTTGCTTATGCAAGACGTCGA 1680  
DB 65571 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGAGACTTGCTTATGCAAGACGTCGA 65512

QY 1681 AACCTTGAATCAGGAGACTCGGATTTCTTTCTGATTCGACATGATGTTGGGTGGAG 1740  
DB 65511 AACCTTGAATCAGGAGACTCGGATTTCTTTCTGATTCGACATGATGTTGGGTGGAG 65452

QY 1741 CGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTGTGCTAATAAGACCTTCA 1800  
DB 65451 CGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTGTGCTAATAAGACCTTCA 65392

QY 1801 GCTCTGCTGTCTGTGAACACTTCCCTGTGATTTCTCTGTGAGGGGGATTTTGAAGGGG 1860  
DB 65391 GCTCTGCTGTCTGTGAACACTTCCCTGTGATTTCTCTGTGAGGGGGATTTTGAAGGGG 65332

QY 1861 AAGGAGCAGAGCTGAGCACTGAGCAAGGGAGGTGAGGGGGAAGAAAGGACAG 1920

Db	65331	AAGAGGCAAGAGCTCGAGAGCAAGCTGAGACACACAGGGAGGTGGAGGGGGAGACAGAAAGCAGG	65272
Oy	1921	CAGAAAGCTGGGTGCTCCATCAGTCTCTCATCTGATCAGCTCAGACTCCAGGACCGAGAGCCA	1980
Db	65271	CAGAAAGCTGGGTGCTCCATCAGTCTCTCATCTGATCAGCTCAGACTCCAGGACCGAGAGCCA	65212
Oy	1881	CAATGCTTCAGAAAGCTCAATGACCCAAAGCCCAATTTTCCTTCCTTAAGCATTAAC	2040
Db	65211	CAATGCTTCAGAAAGCTCAATGACCCAAAGCCCAATTTTCCTTCCTTAAGCATTAAC	65152
Oy	2041	AATGGCAATTTGGCCAACTAAACAAAAGATGACAGACTAACTGATGGTGGCTTTGGCCGT	2100
Db	65151	AATGGCAATTTGGCCAACTAAACAAAAGATGACAGACTAACTGATGGTGGCTTTGGCCGT	65092
Oy	2101	GCATTTCAAAAATGAGGCACAGAGCAAGTGGAAAAATGCCAGAGATTTGTAAACATTTTCAACC	2160
Db	65091	GCATTTCAAAAATGAGGCACAGAGCAAGTGGAAAAATGCCAGAGATTTGTAAACATTTTCAACC	65032
Oy	2161	TGACCAAGCACCCACGACAGCTCAGCAGTGACTGTGACAGACAGAGTGACTTGCAGAGCC	2220
Db	65031	TGACCAAGCACCCACGACAGCTCAGCAGTGACTGTGACAGACAGAGTGACTTGCAGAGCC	64972
Oy	2221	AGGGAGGAGAGAAAAAGAGAGGAGATAGTATGACAGAAAGACAGATTCATTTCAAG	2280
Db	64971	AGGGAGGAGAGAAAAAGAGAGGAGATAGTATGACAGAAAGACAGATTCATTTCAAG	64912
Oy	2281	GGCAGTGGGAATTGACCAAGAGATTATAGTCCACGTGATCTGTGGTTCTAGAGAGCAGG	2340
Db	64911	GGCAGTGGGAATTGACCAAGAGATTATAGTCCACGTGATCTGTGGTTCTAGAGAGCAGG	64852
Oy	2341	GCTATATTTGTGGGGGAAAAATCATGTTCAAGGAAAGTGGGAGACTGTATTTCTAATAC	2400
Db	64851	GCTATATTTGTGGGGGAAAAATCATGTTCAAGGAAAGTGGGAGACTGTATTTCTAATAC	64792
Oy	2401	TATATTTTTCTTTTCAAGCTGAGTATTTCTGAGCAAGTCAACAAGTAGTAACTGAGGCT	2460
Db	64791	TATATTTTTCTTTTCAAGCTGAGTATTTCTGAGCAAGTCAACAAGTAGTAACTGAGGCT	64732
Oy	2461	GTAAGATTACTAGTTTCTCCTTATTAGGAATCTTTTCTCTGTGAGTTAGACAGACA	2520
Db	64731	GTAAGATTACTAGTTTCTCCTTATTAGGAATCTTTTCTCTGTGAGTTAGACAGACA	64672
Oy	2521	AGGGCAATCCGGTTCTTTTAAACGAGAAACAACTTCTTAAAGTAAAGCCAAACAGAT	2580
Db	64671	AGGGCAATCCGGTTCTTTTAAACGAGAAACAACTTCTTAAAGTAAAGCCAAACAGAT	64612
Oy	2581	TCAAGCCATAGCTCTTGCTGAGTAAATAGATTTGTTTTTGAATAATCAATTCAGCCAGTGT	2640
Db	64611	TCAAGCCATAGCTCTTGCTGAGTAAATAGATTTGTTTTTGAATAATCAATTCAGCCAGTGT	64552
Oy	2641	TACTATCTGATTCAGAAAAATGAGACTAGTACCCCTTGGTCAAGCTGTAAACAAACCCAT	2700
Db	64551	TACTATCTGATTCAGAAAAATGAGACTAGTACCCCTTGGTCAAGCTGTAAACAAACCCAT	64492
Oy	2701	TTGTAAATGTCTCAAGTTCAGGCTTAACTGACAAACCAATCAATAAAGATAGAAATCTTT	2760
Db	64491	TTGTAAATGTCTCAAGTTCAGGCTTAACTGACAAACCAATCAATAAAGATAGAAATCTTT	64432
Oy	2761	AGAGCAAACTGTGTTTCTCCACTCTGAGAGTGAATCTGCCAGGGCAAGTTGGAAATATT	2820
Db	64431	AGAGCAAACTGTGTTTCTCCACTCTGAGAGTGAATCTGCCAGGGCAAGTTGGAAATATT	64372
Oy	2821	ACTTACAAGATTGACAGCTGTGTGGTATTACAACATPAAGTTGCTCAAGGGCAATC	2880
Db	64371	ACTTACAAGATTGACAGCTGTGTGGTATTACAACATPAAGTTGCTCAAGGGCAATC	64312
Oy	2881	ATTATTTCAAGTGGCTTAAAGTTAACTTCTGACAGTTTGGTATTAATTAATGCTATTTGCC	2940
Db	64311	ATTATTTCAAGTGGCTTAAAGTTAACTTCTGACAGTTTGGTATTAATTAATGCTATTTGCC	64252
Oy	2941	ATTGCTTTTGTGTTTTTCTCTTTGGTTTATATGTAAAGCAGGGATTTATTAACCTAC	3000
Db	64251	ATTGCTTTTGTGTTTTTCTCTTTGGTTTATATGTAAAGCAGGGATTTATTAACCTAC	64192

QY	3001	AGTCCGAAAGCCTGTGAAATTGTAATGAGGAAAAATTACATTTTGTGTTTTCACACCTT	3060
Db	64191	AGTCCGAAAGCCTGTGAAATTGTAATGAGGAAAAATTACATTTTGTGTTTTCACACCTT	64132
QY	3061	CTAACCTAAATTAAACATTTTATTCATTTGCGCAATGAGCCATPAACCTGAAGGTGAATA	3120
Db	64131	CTAACCTAAATTAAACATTTTATTCATTTGCGCAATGAGCCATPAACCTGAAGGTGAATA	64072
QY	3121	ACAGTACTGTGATTTTGTGATTCATTAACCAATAGAAATCACAGACATTTTACTATATTACA	3180
Db	64071	ACAGTACTGTGATTTTGTGATTCATTAACCAATAGAAATCACAGACATTTTACTATATTACA	64012
QY	3181	GTTGTGTGACAGATAGCTGTGAAGTGAATAATTATATCTCAAACTATCTTTGAAATTAGACC	3240
Db	64011	GTTGTGTGACAGATAGCTGTGAAGTGAATAATTATATCTCAAACTATCTTTGAAATTAGACC	63952
QY	3241	TCCGTGCGGATCTTGTGTTTAACTATTAATAAATCATGTTAAATTTGATATTGTA	3300
Db	63951	TCCGTGCGGATCTTGTGTTTAACTATTAATAAATCATGTTAAATTTGATATTGTA	63892
QY	3301	TAAATCATATTCAATTATCAATTTGTTTCCCTTGTAACTATATTTATTTATTTGAAAAACA	3360
Db	63891	TAAATCATATTCAATTATCAATTTGTTTCCCTTGTAACTATATTTATTTATTTGAAAAACA	63832
QY	3361	TCCTTCTGAGAGAGTTCCCCAGATTTCCACAAATGAGTTCTTGCGATGCAACACACAG	3420
Db	63831	TCCTTCTGAGAGAGTTCCCCAGATTTCCACCAATGAGTTCTTGCGATGCAACACACAG	63772
QY	3421	AGTAAAGACGATTTTGAAGGCTTAACTTAACTATGCTGTGAGATGCAAGCTGAATTT	3480
Db	63771	AGTAAAGACGATTTTGAAGGCTTAACTTAACTATGCTGTGAGATGCAAGCTGAATTT	63712
QY	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTGAAGGGGAAATCTGC	3540
Db	63711	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTGAAGGGGAAATCTGC	63652
QY	3541	CGCTTCTAATAGGAATGCTCTCCCTGAGGCTGTGAAGGTGCTGCTTGTGTTCTGCGCTG	3600
Db	63651	CGCTTCTAATAGGAATGCTCTCCCTGAGGCTGTGAAGGTGCTGCTTGTGTTCTGCGCTG	63592
QY	3601	GCTGTATTTTCTCTGTCCCTGCTACGTCCTTAAAGACCTTGTGTAATCTCCATTTCT	3660
Db	63591	GCTGTATTTTCTCTGTCCCTGCTACGTCCTTAAAGACCTTGTGTAATCTCCATTTCT	63532
QY	3661	AGCATATGCTGCGCACAGTGCAGGTTCTCAATGAATTTTGACAGATGAAATGAAATATA	3720
Db	63531	AGCATATGCTGCGCACAGTGCAGGTTCTCAATGAATTTTGACAGATGAAATGAAATATA	63472
QY	3721	ACTAGAAATATATCTCTGTGTAATGACACACACAGTATCTCGGTGAAGTGTGTAC	3780
Db	63471	ACTAGAAATATATCTCTGTGTAATGACACACACAGTATCTCGGTGAAGTGTGTAC	63412
QY	3781	GTTGTGTGTGTGTGTGTGTGTGTGTAAACAGGTGAGATATATGAACTATATTTGGG	3840
Db	63411	GTTGTGTGTGTGTGTGTGTGTGTGTAAACAGGTGAGATATATGAACTATATTTGGG	63352
QY	3841	GTAATGGGTGCAATAATTGGATGTTCTTTTAAAGAAATCCAAACAGACTTCGTGAA	3900
Db	63351	GTAATGGGTGCAATAATTGGATGTTCTTTTAAAGAAATCCAAACAGACTTCGTGAA	63292
QY	3901	GATTATTTTCTPAAGATCTTGCTGCGCAGCTGAAAGGCAACCCCTGTGCAACGCCAC	3960
Db	63291	GATTATTTTCTPAAGATCTTGCTGCGCAGCTGAAAGGCAACCCCTGTGCAACGCCAC	63232
QY	3961	CCAGCTCACGTGCGCACTCTGTCTTCCCCATGAAAGGCTGTGCTCCCAAGTATATATA	4020
Db	63231	CCAGCTCACGTGCGCACTCTGTCTTCCCCATGAAAGGCTGTGCTCCCAAGTATATATA	63172
QY	4021	AACCTCTCTGGAAGTCTCAGGCAATGAGCCAGAAAGGCCACCATTCACAGGCACTCTCAGCAC	4080
Db	63171	AACCTCTCTGGAAGTCTGGAATGAGCCAGAAAGGCCACCATTCACAGGCACTCTCAGCAC	63112

QY 4081 AGCAGAGCTTCCAGAGAAACCTCAACAACTCTGCAATGAGGTTCTTCTGTGACGCT 4140  
 DB 63111 AGCAGAGCTTCCAGAGAAACCTCAACAACTCTGCAATGAGGTTCTTCTGTGACGCT 63052  
 QY 4141 TGCCTGAGCTTTGGGCGCTGAGATGCGACGCTGCTCAAGTGTGCTTCTGCGCTGCTGCTG 4200  
 DB 63051 TGCCTGAGCTTTGGGCGCTGAGATGCGACGCTGCTCAAGTGTGCTTCTGCGCTGCTGCTG 62992  
 QY 4201 TGGGATGTGGGGGCGCAGAGAGCTCAGCTCAGAGAGGCGCAATGACAGAGTGGCGGATG 4260  
 DB 62991 TGGGATGTGGGGGCGCAGAGAGCTCAGCTCAGAGAGGCGCAATGACAGAGTGGCGGATG 62932  
 QY 4261 CAGTATACCTTCACTGTGCGCACTCCCAATGAATCCAGCTGCCAAGCAGAGCAGAGCC 4320  
 DB 62931 CAGTATACCTTCACTGTGCGCACTCCCAATGAATCCAGCTGCCAAGCAGAGCAGAGCC 62872  
 QY 4321 ATGTGAGTATCCATTAATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380  
 DB 62871 ATGTGAGTATCCATTAATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62812  
 QY 4381 ACCAAGCTGAGCTCAGCTCCTGAGAGAGCTCCTCAACCAATTTGACCTTGAACAGGCT 4440  
 DB 62811 ACCAAGCTGAGCTCAGCTCCTGAGAGAGCTCCTCAACCAATTTGACCTTGAACAGGCT 62752  
 QY 4441 GCCAGGCCCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4500  
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 Homnidae; Homo.  
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 REFERENCES  
 1. Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 1, clone RP11-138F3  
 JOURNAL Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 170425)  
 Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,  
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TITLE  
JOURNAL  
COMMENT

Direct Submission  
 Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 25, 2000 this sequence version replaced gi:17249345.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR

Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L7153

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
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 Quality coverage: 4.1 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 28 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

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ACCESSION ARI23665
VERSION   ARI23665.1 GI:14109026
KEYWORDS
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ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 6169)
AUTHORS  Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.
TITLE     Methods for the diagnosis, prognosis and treatment of glaucoma and
related disorders
JOURNAL   Patent: US 6171788-A 3 09-JAN-2001;
FEATURES  Location/Qualifiers
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           /mol_type="unassigned DNA"

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Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;

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Qy      121 AACCTGTGCTCCAGGTTCAAGCAATTCCTCGTCTGACGCTCCCGGAGTAGTGGAGT 180
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ACCESSION  
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VERSION  
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KEYWORDS  
JP 2002534135-A/3.  
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ORGANISM  
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Hominoidea; Homo.

REFERENCE  
1 (bases 1 to 6169)  
Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
Nucleic acids, kits, and methods for the diagnosis, prognosis and  
treatment of glaucoma and related disorders  
Patent: JP 2002534135-A 3 15-OCT-2002

JOURNAL  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
OS Homo sapiens (human)  
PN JP 2002534135-A/3  
PD 15-OCT-2002  
PE 11-JAN-2000 JP 2000593777  
PR 11-JAN-1999 US 09/227881, 07-MAY-1999 US 09/306828 PI

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 Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
 Nucleic acids, kits, and methods for the diagnosis, prognosis and  
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ACCESSION AR123663  
VERSION AR123663.1 GI:14109024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 5300)  
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
TITLES Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders  
JOURNAL Patent: US 6171788-A 1 09-JAN-2001;  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 67.8%; Score 4069.4; DB 6; Length 5300;  
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QY 3421 AGTAAGAACTGATTTAAGGCTTAACATTTGACATTTGTCCTGAGATGACAGCTGAATT 3480  
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Db 4696 AGAAAGTTCTCCCAAGATTAACAGTGTGTTTAAAGCTAAGGGGTGAAGGGGAAAAATCTGC 4755  
QY 3541 CGCTTCTAATGAAGATCTCTCCCTGAGCCTGTAGGGGCTGTCTTGTGTGCTGGGCTG 3600  
Db 4756 CGCTTCTAATGAAGATCTCTCCCTGAGCCTGTAGGGGCTGTCTTGTGTGCTGGGCTG 4815  
QY 3601 GCTGTAAATTTTCTCTGTCTCTGCTGTAAGCTTTAAAGACTGTGTTGAATCTCAAGTTCT 3660  
Db 4816 GCTGTAAATTTTCTCTGTCTCTGCTGTAAGCTTTAAAGACTGTGTTGAATCTCAAGTTCT 4875



QY 1021 GGGCACTCCCTAGCGGCCCCCTGCTGCCTCATCTGTCCCGAGGCCCCCAAGCCGAGT 1080  
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QY 1081 CTTCAGAGCCCTCCCTCATCACTGTCACAGGCTGCGAGCTGCGCTGCTGCTTCCCGT 1140  
Db 2296 CTTCAGAGCCCTCCCTCATCACTGTCACAGGCTGCGAGCTGCGCTGCTGCTTCCCGT 2355  
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Db 2356 AATGCTCTGTGATCTGAGCTGAGAGCTCTTGTGCTCCAGGCTCCAGAAAGGAATGG 2415  
QY 1201 AGAGGAAACTAGTCTAACGGAATCTGAGGGGACAGTGTTCCTCAGAGGAAAGG 1260  
Db 2416 AGAGGAAACTAGTCTAACGGAATCTGAGGGGACAGTGTTCCTCAGAGGAAAGG 2475  
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QY 1321 TGAGCGGCTCTGAAAGGAGAGGAAAGGAGGAGGCTGAGAGCTGCGCAGATGTC 1380  
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QY 1381 AGTGTGTTCAAGGAGCTGGAAGTTCGCTGCTCTGAGAGCTTTTATCTTTCT 1440  
Db 2596 AGTGTGTTCAAGGAGCTGGAAGTTCGCTGCTCTGAGAGCTTTTATCTTTCT 2655  
QY 1441 CTGCTTGAGAGAGAAAGTCTATTCTATGAGAGATGAGTTTCATTAAGTCACTGTT 1500  
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Db 2716 AAAATTCAGAGGCTGATGGTTCCTTCAAGAGGCTTTATTTAATGGAAATAG 2775  
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QY 1681 AACCTTGAAATCAGAGACTCGGTTTCTTCTGTTCTGCTGCAATGGTTGGCTGTGCA 1740  
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QY 1861 AAGAGGAGAGAGCTGAGAGAGTCAAGGGAGGTGAGGGGAGAGAGAGGCAAG 1920  
Db 3076 AAGAGGAGAGAGCTGAGAGAGTCAAGGGAGGTGAGGGGAGAGAGAGGCAAG 3135  
QY 1921 CAGAACTGGTCTCATCATGTCTCACTGATCACTGAGACTCCAGAGCCGAGAGCA 1980  
Db 3136 CAGAACTGGTCTCATCATGTCTCACTGATCACTGAGACTCCAGAGCCGAGAGCA 3195  
QY 1981 CAATGCTTCAAGAAAGCTCAATGAAACCAAGCCCAATTTTCTTCCCTAAGCATAGAC 2040  
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QY 2041 AATGCAATTTGCAATTAACCAAAAGATGAGAGACTAAGTGTGATGCTTTGGCG 2100  
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QY 2461 GTAGATTACTTAGTTCCTCTAATTAGAGACTTTTCTCTGTGAGTTAGCAGACA 2520  
Db 3676 GTAGATTACTTAGTTCCTCTAATTAGAGACTTTTCTCTGTGAGTTAGCAGACA 3735  
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QY 2821 ACTTCAAGATTAAGACTGTGTGTGATTAACAATTAAGTTGCTCAAGGCAATC 2880  
Db 4036 ACTTCAAGATTAAGACTGTGTGTGATTAACAATTAAGTTGCTCAAGGCAATC 4095  
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QY 3121 ACAGTACCTGTGATTTGTCAATTAACCAATTAAGCAATTTTATCTATTAATTA 3180  
Db 4336 ACAGTACCTGTGATTTGTCAATTAACCAATTAAGCAATTTTATCTATTAATTA 4395  
QY 3181 GTTGTGAGATAGCTGTGAAGTAATTAATTAATCAATTAATTAATTAATTAATTA 3240



[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
1	(bases 1 to 5300)				
	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders	Patent: US 6475724-A 1 05-NOV-2002;	The Regents of the University of California; Oakland, CA	
				Location/Qualifiers	
				1..5300	
				/organism="unknown"	
				/mol_type="genomic DNA"	
Query Match	67.8%;	Score 4069.4;	DB 6;	Length 5300;	
Best Local Similarity	99.9%;	Pred. No. 0;			
Matches 4082;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 1;	
QY	1	GCTCCACAGGAAGTCTCCCACTCTAGACTTCTGCATCAGATGTTACAGCCAGAAAGTCC	60		
DB	1216	GCTCCACAGGAAGTCTCCCACTCTAGACTTCTGCATCAGATGTTACAGCCAGAAAGTCC	1275		
QY	61	CGTGAAGGTGAGGCTCTGTCTTCAACCTACCTGATAGCTCTACCTGAGCTCACTGC	120		
DB	1276	CGTGAAGGTGAGGCTCTGTCTTCAACCTACCTGATAGCTCTACCTGAGCTCACTGC	1335		
QY	121	AACCTGCTCCCAAGGTTCAAGCAATCTCTGCTCAGCCTCCGGTAGCTGGAGCT	180		
DB	1336	AACCTGCTCCCAAGGTTCAAGCAATCTCTGCTCAGCCTCCGGTAGCTGGAGCT	1399		
QY	181	ACAGCGCAGCCCGGCTAATTTTTGTATTTGTATGTAGAGATGGGGTTCAACATATTAG	240		
DB	1396	ACAGCGCAGCCCGGCTAATTTTTGTATTTGTATGTAGAGATGGGGTTCAACATATTAG	1455		
QY	241	CCCGGCTGCTTGAACCTCTGACTCTCAGGTGATCCACCACCTCAGCTCTTAAAGTGC	300		
DB	1456	CCCGGCTGCTTGAACCTCTGACTCTCAGGTGATCCACCACCTCAGCTCTTAAAGTGC	1515		
QY	301	TGGGATTACAGGATGAGTCAACCGGCGCCGAGGAGGCTAGTGTATTAAGAAATTAAC	360		
DB	1516	TGGGATTACAGGATGAGTCAACCGGCGCCGAGGAGGCTAGTGTATTAAGAAATTAAC	1575		
QY	361	TTGAATGGTTTACTTAAACCAACAGGAAACAGACAAAGCTGTGTAAATTCAGGAATTC	420		
DB	1576	TTGAATGGTTTACTTAAACCAACAGGAAACAGACAAAGCTGTGTAAATTCAGGAATTC	1635		
QY	421	TTGGATGGGGAATGTGTCATGAGCTGCTGCTTAATGCCAGACCACTGGTCTCATCA	480		
DB	1636	TTGGATGGGGAATGTGTCATGAGCTGCTGCTTAATGCCAGACCACTGGTCTCATCA	1691		
QY	481	CTTCTCCCTCATCTCATTTTTCAGGCTAAGTACCAATTTATTCACCAATCTTTTGTG	540		
DB	1696	CTTCTCCCTCATCTCATTTTTCAGGCTAAGTACCAATTTATTCACCAATCTTTTGTG	1751		
QY	541	GTAAGCCTCCACATCGTTACTGAAATTAAGATATCATTAACCTAGTTCATTTGGGCCCA	600		
DB	1756	GTAAGCCTCCACATCGTTACTGAAATTAAGATATCATTAACCTAGTTCATTTGGGCCCA	1811		
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DB	1816	TCTGTGTGTGTATTAAGGGAAGAGGCAATCCCAAGACCTCTTGAAGCCCCCGGACG	1871		
QY	661	AAGTTCCTCTCCACATCGGGGGAAGCCCTGCAAGCAACCGGGGTCCTGGGTGTCTGAGCA	720		
DB	1876	AAGTTCCTCTCCACATCGGGGGAAGCCCTGCAAGCAACCGGGGTCCTGGGTGTCTGAGCA	1931		
QY	721	ACCTGCAAGCCGCTGCACTGGTTGTTTGTATCATCTCTAGAGCACTGTGTGCTTCT	780		
DB	1936	ACCTGCAAGCCGCTGCACTGGTTGTTTGTATCATCTCTAGAGCACTGTGTGCTTCT	1991		
QY	781	ATTTCGTGTGACTGTTCAATTCAGGCAATTCATGAACATTTATTAAGTACTTATA	840		
DB	1996	ATTTCGTGTGACTGTTCAATTCAGGCAATTCATGAACATTTATTAAGTACTTATA	2051		
QY	841	TCTGCCAGACCAAGAGCAAAATGTTAGCAAGCAATCTGCCCTACCTTCGTGGAG	900		

Dp	2056	TTGGCAAGACACACAGACAAAATGTAAGCAAGCACTCATCTGCTTACCTTGATGAG	2115
Qy	901	GTGACAGTTTCTCATGGAAGAAGTCAGAAAGAAATTAATAGCCAGCACTTAAACCA	960
Dp	2116	GTGACAGTTTCTCATGGAAGAAGTCAGAAAGAAATTAATAGCCAGCACTTAAACCA	2175
Qy	961	GTGCTGAAAGAAAGAAATTAACACCAATCTTGAGAAATTGTGCGAGCATCCCTTAA	1020
Dp	2176	GTGCTGAAAGAAAGAAATTAACACCAATCTTGAGAAATTGTGCGAGCATCCCTTAA	2235
Qy	1021	GGCAGCTCCCTTAAGGGCCCCGTCGCTCCATGCTGTGCCGGAAGCCCCCAAGCCAGT	1080
Dp	2236	GGCAGCTCCCTTAAGGGCCCCGTCGCTCCCTTAAGCTGTGCCGGAAGCCCCCAAGCCAGT	2295
Qy	1081	CTTCCAAAGCTCTCTCTCCATCATGTCAGAGCGCTCACTAGACCTGCTTCCCGTG	1140
Dp	2296	CTTCCAAAGCTCTCTCTCCATCATGTCAGAGCGCTCACTAGACCTGCTTCCCGTG	2355
Qy	1141	AATCGTCTGTGTGCAATCTGAGCTGAGACTCTCTTGCTTCCAGGCTCCAGAAAGAAATGG	1200
Dp	2356	AATCGTCTGTGTGCAATCTGAGCTGAGACTCTCTTGCTTCCAGGCTCCAGAAAGAAATGG	2415
Qy	1201	AGAGGGAATCTAGTCTTAACGGAATCTGGAAGGGGACAGTGTTCCTCAAGGGGAAAGG	1260
Dp	2416	AGAGGGAATCTAGTCTTAACGGAATCTGGAAGGGGACAGTGTTCCTCAAGGGGAAAGG	2475
Qy	1261	GCCTCCAGTCCAGAGAAATTCAGAGAAGTGGGACCTGCAAGAGTGGGGACGCTGGGGC	1320
Dp	2476	GCCTCCAGTCCAGAGAAATTCAGAGAAGTGGGACCTGCAAGAGTGGGGACGCTGGGGC	2535
Qy	1321	TGAGCGGGTGCTGAAGGACGAGAAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAATGTTC	1380
Dp	2536	TGAGCGGGTGCTGAAGGACGAGAAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAATGTTC	2595
Qy	1381	AGTGTGTTCACGGGGCTGGGAGTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT	1440
Dp	2596	AGTGTGTTCACGGGGCTGGGAGTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT	2655
Qy	1441	CTGCTTGAAGAGAAAGTCTAATTCAATGAAGGATGCAATTCATTAATGACGCTGT	1500
Dp	2656	CTGCTTGAAGAGAAAGTCTAATTCAATGAAGGATGCAATTCATTAATGACGCTGT	2715
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Dp	2716	AAAATTCAGGGTGTCATGAGGTTCCTTACAGAAAGGCTTTAATTAATGGAAATAG	2775
Qy	1561	GAAGGAGCTCATTTCTTAAGCCGTTAATTCACGAGAAAGTGAAGTGAAGTCTTTCTTT	1620
Dp	2776	GAAGGAGCTCATTTCTTAAGCCGTTAATTCACGAGAAAGTGAAGTGAAGTCTTTCTTT	2835
Qy	1621	CATGCTTCTGGGCAACTACTCAGGCCGTGTGTGAATGGCTTAATGCAAGCGTGA	1680
Dp	2836	CATGCTTCTGGGCAACTACTCAGGCCGTGTGTGAATGGCTTAATGCAAGCGTGA	2895
Qy	1681	AACCTTGAATCAGAGAGCTGAGTTTCTTCTGAGTCTGCAATTTGTTGGCTGTGGAC	1740
Dp	2896	AACCTTGAATCAGAGAGCTGAGTTTCTTCTGAGTCTGCAATTTGTTGGCTGTGGAC	2955
Qy	1741	CGTGGGCAAGTGTCTCTCTTCCGTGGCCATAGCTTTCTCTGCTATTAAGACCCCTTGCA	1800
Dp	2956	CGTGGGCAAGTGTCTCTCTTCCGTGGCCATAGCTTTCTCTGCTATTAAGACCCCTTGCA	3015
Qy	1801	GCTCTCGGTTCTGTGAACATCTCCGTGTGAATTCCTGTGAAGGGGGAATGTGAAGAGG	1860
Dp	3016	GCTCTCGGTTCTGTGAACATCTCCGTGTGAATTCCTGTGAAGGGGGAATGTGAAGAGG	3075
Qy	1861	AAGAGGAGAGCTGAGCAGCTGAGCCACAGGGGAGGTGAAGGGGACAGGAAGGACG	1920
Dp	3076	AAGAGGAGAGCTGAGCAGCTGAGCCACAGGGGAGGTGAAGGGGACAGGAAGGACG	3135
Qy	1921	CAGAAAGCTGGGTCTCATCAAGTCTCATGATCACTGACATTCAGAAACGAGACCA	1980

Db	3136	CAGAAAGCTGGGTGCTCCATCAATGCTCTCACTGATCAAGTCAAGTCTCAAGACCGAGACCA	3195
OY	1981	CAATGCTTCAGGAAGAGCTCAATGAACCAACGACCATTTTCTTCCCTTAAGCATAGAC	2040
Db	3136	CAATGCTTCAGGAAGAGCTCAATGAACCAACGACCATTTTCTTCCCTTAAGCATAGAC	3255
OY	2041	AATGCAATTTGCCAATTAACCAAAAAGATGACAGACTAACTGGTGGTACCTTTTGGCTG	2100
Db	3256	AATGCAATTTGCCAATTAACCAAAAAGATGACAGACTAACTGGTGGTACCTTTTGGCTG	3315
OY	2101	GCATTTCAAAAACCTGGGCGACAGCAAGTGGAAAAATCCAGAGATTGTTTAACTTTTCAACC	2160
Db	3316	GCATTTCAAAAACCTGGGCGACAGCAAGTGGAAAAATCCAGAGATTGTTTAACTTTTCAACC	3375
OY	2161	TGACCAGACCCCAAGCAGAGCTCAGCAGTGAATCTGTCACACACGAGTGAATCTTGACGCG	2220
Db	3376	TGACCAGACCCCAAGCAGAGCTCAGCAGTGAATCTGTCACACACGAGTGAATCTTGACGCG	3435
OY	2221	AGGGAGAGAGAAAAAAGAGAGGATAGTATGACAAAGAAAGACAGATTCAATTCAG	2280
Db	3436	AGGGAGAGAGAAAAAAGAGAGGATAGTATGACAAAGAAAGACAGATTCAATTCAG	3495
OY	2281	GGCAGTGGGAATTACCAACAGGATTTAATGCCAGTGAATCTTGAGTGAAGGACGAG	2340
Db	3496	GGCAGTGGGAATTACCAACAGGATTTAATGCCAGTGAATCTTGAGTGAAGGACGAG	3555
OY	2341	GCTATATTTGGGGGGAAAAAATCAGTTCAAGGGAAGTGGGGAGACCTGATTTCTAATAC	2400
Db	3556	GCTATATTTGGGGGGAAAAAATCAGTTCAAGGGAAGTGGGGAGACCTGATTTCTAATAC	3615
OY	2401	TATATTTTTCTTTTACCAAGCTGAGTATTTCTGACAGTCAACAGTATGAATCTGAGGCT	2460
Db	3616	TATATTTTTCTTTTACCAAGCTGAGTATTTCTGACAGTCAACAGTATGAATCTGAGGCT	3675
OY	2461	GTAAGATTACTTAAGTTCTCTTATTGAACTCTTTTCTCTGTGGAGTTAGCAGACA	2520
Db	3676	GTAAGATTACTTAAGTTCTCTTATTGAACTCTTTTCTCTGTGGAGTTAGCAGACA	3735
OY	2521	AGGGCAATCCCGTTCTTTTAAACAGGAAGAAACAATCCCTAAGATGAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTCTTTTAAACAGGAAGAAACAATCCCTAAGATGAAGCCAAACAGAT	3795
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Db	3796	TCAAGCCTAAGTCTTGTCTGACTATATGATTTGGTTTTTGAAAAATCATTTCAAGCATGT	3855
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Db	3916	TTTGAATATGCTCAAGTTCAAGGCTTAACTGACAAACCAATCAANTAAAGATTAATCTTT	3975
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Db	3976	AGAGCAAACTGTGTTTTCTCACTCTGGAGGTGAGCTGACAGGGCAGTTTGGAAATATT	4035
OY	2821	ACTTCACAAGTATGACACTGTGTTGGTATTTAAACAACATTAAGTTGCTCAAGGCAATC	2880
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OY	2881	ATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATTTATTTGGCTAATGGC	2940
Db	4096	ATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATTTATTTGGCTAATGGC	4155
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OY	3001	AGTCACAAGAGCCTGTGAATTTGAATGAGAAAAAATTAATTTTGTTTTTACAACCTT	3060
Db	4216	AGTCACAAGAGCCTGTGAATTTGAATGAGAAAAAATTAATTTTGTTTTTACAACCTT	4275

[illegible]

LOCUS	BD065039	5299 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.				
ACCESSION	BD065039	GI:22610642			
VERSION	BD065039.1	JP 2001509669-A/1.			
KEYWORDS	JP 2001509669-A/1.				
SOURCE	unidentified				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 5299)				
AUTHORS	Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.				
TITLE	Methods for the diagnosis, prognosis and treatment of glaucoma and related disorders				
JOURNAL	Patent: JP 2001509669-A 1 24-JUL-2001; THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
COMMENT	OS Unidentified PN JP 2001509669-A/1 PD 24-JUL-2001 PF 09-JUN-1998 JP 1998532017 PR 26-JUN-1997 US 08/791154,26-SEP-1997 US 08/938669 PI THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC C12N15/12,C12Q1/68,C07K14/47,A61K31/70 CC Strandedness: Single; CC Topology: Linear; CC Methods for the diagnosis, prognosis and treatment of glaucoma CC treatment of glaucoma and related CC disorders FH Key Location/Qualifiers FT source 1..5300 /organism='Unidentified'. FT 1..5299 Location/Qualifiers 1..5299 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'				
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DB	1276	CGTAGAGGTGAGGGCTGTGTCTTAACCTACCTGATAGCTCTACCTGAGCTCACCTGC	1335		
QY	121	AACCTCTGCTCCCAAGTTCAAGCAATCTCTGCTCAGCCTCCGCGTAGCTGGAGCT	180		
DB	1336	AACCTCTGCTCCCAAGTTCAAGCAATCTCTGCTCAGCCTCCGCGTAGCTGGAGCT	1395		
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DB	1456	CCCGGCTGAGTCTTGAACTCCTGACCTCAGTGATCCACCACCTCAGGCTCTTAAAGTGC	1515		
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DB	1516	TGGAGTTACAGGATGAGTCAACCGGCGCCGCGCAAGGGTCAAGTGTATTAATGAATTAAC	1575		
QY	361	TTGATGTGTTTACTTAAACCAACAGGAAACAGAAAGCTGTATTAATTCACGAGATTC	420		
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[illegible]

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Query Match 67.6%; Score 4057.4; DB 6; Length 5304;  
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DB 1276 CGTAGAGGTAGAGGTCTGTGCTTTACACCTACCGTATGCTCTACACCTGAGCTCACTGC 1335  
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ACCESSION BD237935 treatment of glaucoma and related disorders.  
 VERSION BD237935.1 GI:33047705  
 KEYWORDS JP 2002534135-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 5304)  
 Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
 Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders  
 Patent: JP 2002534135-A 2 15-OCT-2002;  
 THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
 OS Homo sapiens (human)  
 PN JP 2002534135-A/2  
 PD 15-OCT-2002  
 PF 11-JAN-2000 JP 2000593777  
 PR 11-JAN-1999 US 09/227881,07-MAY-1999 US 09/306828 PI  
 THAI D NGUYEN, JON R POLANSKY, PU CHEN, HUA CHEN PC  
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 C12N1/21,  
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 and  
 CC treatment of glaucoma and related disorders  
 FH Key Location/Qualifiers  
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ORIGIN

Query Match 67.6%; Score 4057.4; DB 6; Length 5304;  
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 Matches 4077; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

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Query Match	Best Local Similarity	Conservative	Mismatches	Indels	Gaps
67.4%; Score 4044.8; DB 8; Length 5300;	99.9%; Pred. No. 0;	0; Mismatches	2; Indels	4; Gaps	3;
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121 AACCTGCGCCCGCAGGTTCAAGCAATTCCTGCTCAGCCCTCCCGGCTAGAGTGGAGCT 180	1336 AACCTGCGCCCGCAGGTTCAAGCAATTCCTGCTCAGCCCTCCCGGCTAGAGTGGAGCT 1395				
181 ACAGGCGACGCCCCGCTAAATTTTGTATTTAGTATGAGATGAGGGTTTACCAATATTAG 240	1396 ACAGGCGACGCCCCGCTAAATTTTGTATTTAGTATGAGATGAGGGTTTACCAATATTAG 1455				
241 CCCGGCTGCTTGAATCTCCTGACCTCAGGTATCCACCACCTCAGCTCTTAAAGTGC 300	1456 CCCGGCTGCTTGAATCTCCTGACCTCAGGTATCCACCACCTCAGCTCTTAAAGTGC 1515				
301 TGGGATTTACAGGCAATGATGACCGCGCCCGGCGCAAGGCTTACGTTTAATAGGAATAC 360	1516 TGGGATTTACAGGCAATGATGACCGCGCCCGGCGCAAGGCTTACGTTTAATAGGAATAC 1575				
361 TTGATAGGTTTACAAACCAACAGGAGAAAGCAAAAGCTGTATTAATTTACGGGATTC 420	1576 TTGATAGGTTTACAAACCAACAGGAGAAAGCAAAAGCTGTATTAATTTACGGGATTC 1635				
421 TTGGGATGAGGAATGATGTCATGAGCTGCTGCTAGTCCAGACCACTGTCCTCATCA 480	1636 TTGGGATGAGGAATGATGTCATGAGCTGCTGCTAGTCCAGACCACTGTCCTCATCA 1695				
481 CTTTCTTCCTCATCTCTCATATTTTCAAGGCTAAGTTACATTTTATTCACATGCTTTTGTG 540	1696 CTTTCTTCCTCATCTCTCATATTTTCAAGGCTAAGTTACATTTTATTCACATGCTTTTGTG 1755				
541 GTAAGCCTCCACATCGTTACTGAATTAAGATTAATTAATACTAAGTTTCAATTTTGGGCCA 600	1756 GTAAGCCTCCACATCGTTACTGAATTAAGATTAATTAATACTAAGTTTCAATTTTGGGCCA 1815				
601 TCTGTGTGTGTATATAGGGAGAGAGGCAATCCCGAGAGACTCTTGAAGCCCGCGCAG 660	1816 TCTGTGTGTGTATATAGGGAGAGAGGCAATCCCGAGAGACTCTTGAAGCCCGCGCAG 1875				
661 AGGTTTCTCTCCAGCTGAGGGAGAGCCCTGCAAGCAATCCGGGGGCTCTGGGTGTCTTGA 720	1876 AGGTTTCTCTCCAGCTGAGGGAGAGCCCTGCAAGCAATCCGGGGGCTCTGGGTGTCTTGA 1935				
721 ACCGTCAGAGCCCGGCACTGATGTTTGTGTATCACTGCTAAGGAGCCTGTGCTTCTCT 780	1936 ACCGTCAGAGCCCGGCACTGATGTTTGTGTATCACTGCTAAGGAGCCTGTGCTTCTCT 1995				
781 ATTCTGTGTGTACTGTCTTCAATTCATCAGGCAATTCATGACATTTATAGATACTTATA 840	1996 ATTCTGTGTGTACTGTCTTCAATTCATCAGGCAATTCATGACATTTATAGATACTTATA 2055				
841 TCTGCCAGACCAAGAGCAAAATGTTGACAAAGCATCTGCCCTTACCTTGTGAG 900	2056 TCTGCCAGACCAAGAGCAAAATGTTGACAAAGCATCTGCCCTTACCTTGTGAG 2115				
901 GTGACAGTTTCTCATGAGAAAGGTGAGAAAGAAATTAATACCGGCACTTAATACCA 960					

Db 2116 GTGACAGTTTCTCATGGAAGACGTGACAGAAATAATTAATAGCCAGCCACTTAACCCA 2175  
Qy 961 GTGCTGAAAGAAAGAAATAAACCACATCTTGAAGAAATTTGGCCAGCATCCCTTAACA 1020  
Db 2176 GTGCTGAAAGAAAGAAATAAACCACATCTTGAAGAAATTTGGCCAGCATCCCTTAACA 2235  
Qy 1021 GGCCACCTCCCTAGCGCCCCCTGCTGCTCCATCGTGCCCGAGAGCCCCCAAGCCGAGT 1080  
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Db 2296 CTTTCCAAAGCTTCTCTCTCATCATGTCACAGCGCTGCACTGCTGCTGCTGCTGCTGCTG 2355  
Qy 1141 AATGCTCTGTGATCTGAGCTGGAAGCTCTTGCTGCTCCAGCTCCAGAAAGAAATGG 1200  
Db 2356 AATGCTCTGTGATCTGAGCTGGAAGCTCTTGCTGCTCCAGCTCCAGAAAGAAATGG 2415  
Qy 1201 AGAGGAAACTAAGTCTTAACGAGAAATCTGAGAGGACAGTGTTCCTTCAGAGGAAAGGG 1260  
Db 2416 AGAGGAAACTAAGTCTTAACGAGAAATCTGAGAGGACAGTGTTCCTTCAGAGGAAAGGG 2475  
Qy 1261 GCCTTCACGTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGAGTGGGACCTGGGAC 1320  
Db 2476 GCCTTCACGTCCAGAGAAATTCAGAGAGTGGGACCTGCAAGAGTGGGACCTGGGAC 2535  
Qy 1321 TGAGCGGTGCTGAAGGCAAGGATGAAAAAGGCAAGGCTGAAGCTGCCAGATGTTTC 1380  
Db 2536 TGAGCGGTGCTGAAGGCAAGGATGAAAAAGGCAAGGCTGAAGCTGCCAGATGTTTC 2595  
Qy 1381 AGTGTGTTCAAGGCGCTGAGAGTTTCGTTGCTTCCTGAGAGCTTTTATCTTTTCT 1440  
Db 2596 AGTGTGTTCAAGGCGCTGAGAGTTTCGTTGCTTCCTGAGAGCTTTTATCTTTTCT 2655  
Qy 1441 CTGCTTGAAGAGAAAGAGTCTATTCAATGAAGGATGCAATTTATTAAGTCACTGTT 1500  
Db 2656 CTGCTTGAAGAGAGAAAGTCTATTCAATGAAGGATGCAATTTATTAAGTCACTGTT 2715  
Qy 1501 AAAATTCAGAGGTGTCAGAGGTTTTCCTTCAAGAGGCTTTATTAAGGAAATATAG 1560  
Db 2716 AAAATTCAGAGGTGTCAGAGGTTTTCCTTCAAGAGGCTTTATTAAGGAAATATAG 2775  
Qy 1561 GAAGGAGCTCATTTCTAGGCGCTTAATTCACGAGAAAGTCACTGAGTCTTTTCTTT 1620  
Db 2776 GAAGGAGCTCATTTCTAGGCGCTTAATTCACGAGAAAGTCACTGAGTCTTTTCTTT 2835  
Qy 1621 CATGCTTCTGGGCACTACTAGCCCTGTGTGACTTGGCTTAATGCAAGCGGTGCA 1680  
Db 2836 CATGCTTCTGGGCACTACTAGCCCTGTGTGACTTGGCTTAATGCAAGCGGTGCA 2895  
Qy 1681 AACCTTGAATCAGAGACTGGGTTTCTTTCTGCTGCAATGTTGGCTGGGAC 1740  
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Qy 1741 CGTGGGCAAGTCTCTCTCTTCCCTGGGCAATAGTCTTCTGCTAATAAGACCTTTGCA 1800  
Db 2956 CGTGGGCAAGTCTCTCTCTTCCCTGGGCAATAGTCTTCTGCTAATAAGACCTTTGCA 3015  
Qy 1801 GCTCTGCTGTCTGTAACAATTCCCTGTGATTTCTGTGAGGGGAGATGTTGAAGGGG 1860  
Db 3016 GCTCTGCTGTCTGTAACAATTCCCTGTGATTTCTGTGAGGGGAGATGTTGAAGGGG 3075  
Qy 1861 AAGGAGGCAAGCTGAGAGCTGAGGCAAGGGGAGGTGAGGGGAGAGAAAGGACG 1920  
Db 3076 AAGGAGGCAAGCTGAGAGCTGAGGCAAGGGGAGGTGAGGGGAGAGAAAGGACG 3135  
Qy 1921 CAGAACTGGTGTCTCATCACTCTCATCTGATCTCACTGAGCTCCAGAGCCGAGAGCCA 1980  
Db 3136 CAGAACTGGTGTCTCATCACTCTCATCTGATCTCACTGAGCTCCAGAGCCGAGAGCCA 3195  
Qy 1981 CAATGCTTCAAGAAAGCTCAATGAACCCAGACCAATTTTCTTCCCTTAAGCATATAGC 2040  
Db 3196 CAATGCTTCAAGAAAGCTCAATGAACCCAGACCAATTTTCTTCCCTTAAGCATATAGC 3255

Qy 2041 AATGCAATTTGCCAATTAACCAAAAAGATGACAGACTAACTGTGTAGCTTTTGCTG 2100  
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Qy 2101 GCATTTCAAAAATGCGGCCAGAGCAAGTGGAAAAATGCCAGAGATTGTTTAACTTTTCA 2160  
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Qy 2581 TCAAGCTAGGCTCTGCTGACTATATGATGGTTTTTGAAGAAATCAATTCAGCGATGT 2640  
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Qy 2641 TACTATCTGATTCAGAAAAATGAGACTAGTACCCTTTGGTGCCTGTAAACAAACCCAG 3915  
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Qy 2701 TTTGAATGCTCAAGTTCAAGGCTTAACTGCAAGAACCAATCAATTAAGATAGATCTTT 2760  
Db 3974 TTTGAATGCTCAAGTTCAAGGCTTAACTGCAAGAACCAATCAATTAAGATAGATCTTT 3974  
Qy 2761 AGAGCAAACTGTGTTCTCCAC-TCTGAGAGTGAAGTGCAGAGGCAAGTTGAAATAT 2819  
Db 3975 AGAGCAAACTGTGTTCTCCAC-TCTGAGAGTGAAGTGCAGAGGCAAGTTGAAATAT 4034  
Qy 2820 TACTTCAAGATTTGACACTGTTGTTGATTAACAACATTAAGTTGCTCAAGGCAAT 2879  
Db 4035 TACTTCAAGATTTGACACTGTTGTTGATTAACAACATTAAGTTGCTCAAGGCAAT 4094  
Qy 2880 CATATTTCAAGTGGCTTAAGTACTTGTGACAGTTTGGTATATTAATGAGCAATGGC 2939  
Db 4095 CATATTTCAAGTGGCTTAAGTACTTGTGACAGTTTGGTATATTAATGAGCAATGGC 4154  
Qy 2940 CATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAGAGAGGATTTAACTTA 2999  
Db 4155 CATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAGAGAGGATTTAACTTA 4214  
Qy 3000 CAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTTTTACACCT 3059  
Db 4215 CAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATTAATTTTGTTTTACACCT 4274  
Qy 3060 TCTAATTAATTTAATTTTATTTTCAATTTGGAATTAAGCATTAACCTCAAGTGTAT 3119  
Db 4275 TCTAATTAATTTAATTTTATTTTCAATTTGGAATTAAGCATTAACCTCAAGTGTAT 4334

QY 3120 AACGTAACCTGTGATTTTGTCAATACCAATAGAAATCAGACATTTTATATATATAC 3179  
DB 4335 AACAGTAACCTGTGATTTTGTCAATACCAATAGAAATCAGACATTTTATATATATAC 4394  
QY 3180 AGTTGTGAGATACGTGTGAAGTAATTTTACTCAAACTACTTTGAAATTAGAC 3239  
DB 4395 AGTTGTGAGATACGTGTGAAGTAATTTTACTCAAACTACTTTGAAATTAGAC 4454  
QY 3240 CTCCTGCTGATCTGTGTTTAAACATTAATTAACATGTTTAAATTTGATTTTG 3299  
DB 4455 CTCCTGCTGATCTGTGTTTAAACATTAATTAACATGTTTAAATTTGATTTTG 4514  
QY 3300 ATATCATATTTCAATATCATTTGTTCTTTGTAATCTATATTTATATATTTGAAAC 3359  
DB 4515 ATATCATATTTCAATATCATTTGTTCTTTGTAATCTATATTTATATATTTGAAAC 4574  
QY 3360 ATCTTCTGAGAGAGTTCCTCCAGATTTTCAATGAGTTCTTGCGATGACACACACA 3419  
DB 4575 ATCTTCTGAGAGAGTTCCTCCAGATTTTCAATGAGTTCTTGCGATGACACACACA 4634  
QY 3420 GAGTAAGAACTGATTTAGAGGCTAACATGACATGCGCTGAGATGCAAGACTGAAT 3479  
DB 4635 GAGTAAGAACTGATTTAGAGGCTAACATGACATGCGCTGAGATGCAAGACTGAAT 4694  
QY 3480 TAGAAAGTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGTGAGGGGGGAAATCTG 3539  
DB 4695 TAGAAAGTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGTGAGGGGGGAAATCTG 4754  
QY 3540 CCGCTTCTATAGAAATGCTCTCCCTGAGGCTGGTAGGGTGCTGCTGTGTTTGCT 3599  
DB 4755 CCGCTTCTATAGAAATGCTCTCCCTGAGGCTGGTAGGGTGCTGCTGTGTTTGCT 4814  
QY 3600 GGGCTGTAATTTTCTGTCCTGCTACGCTTAAAGGACTTGTGGAATCTCCAGTCC 3659  
DB 4815 GGGCTGTAATTTTCTGTCCTGCTACGCTTAAAGGACTTGTGGAATCTCCAGTCC 4874  
QY 3660 TAGCATAGTGCCTGAGCAGTGCAGGTTCTCAATGAGTTGACAGTGAATGGAATATA 3719  
DB 4875 TAGCATAGTGCCTGAGCAGTGCAGGTTCTCAATGAGTTGACAGTGAATGGAATATA 4934  
QY 3720 AACTAGAAATATATCTTGTGTAATCAGACACCAATGCTCTGCTGTAAGTGTGTGA 3779  
DB 4935 AACTAGAAATATATCTTGTGTAATCAGACACCAATGCTCTGCTGTAAGTGTGTGA 4994  
QY 3780 C--GTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAGATATAGGAATATATT 3837  
DB 4995 CGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAGATATAGGAATATATT 5054  
QY 3838 GGGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTG 3897  
DB 5055 GGGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTG 5114  
QY 3898 GAAAGTATTTTCTAAGAACTTTGCTGCAAGCGTGAAGGCAACCCCTGTGCAAGCCC 3957  
DB 5115 GAAAGTATTTTCTAAGAACTTTGCTGCAAGCGTGAAGGCAACCCCTGTGCAAGCCC 5174  
QY 3958 CACCAGCCTCAAGTGGCAACCTGTCTCCGCCATGAAGGCTGGCTCCCAATATAT 4017  
DB 5175 CACCAGCCTCAAGTGGCAACCTGTCTCTTCCCAATGAAGGCTGGCTCCCAATATAT 5234  
QY 4018 ATTAACCTTCTGAGCTGAGGATGAGCAGCAAGGCAACCATCAGGCACTTCTGAG 4077  
DB 5235 ATTAACCTTCTGAGCTGAGGATGAGCAGCAAGGCAACCATCAGGCACTTCTGAG 5294  
QY 4078 CACAGC 4083  
DB 5295 CACAGC 5300



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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 01:06:29 ; Search time 3207 Seconds  
(without alignments)  
12469.023 Million cell updates/sec

SEQ1-4037A

Title: SEQ1-4037A  
Perfect score: 6000  
Sequence: 1 gctccacaggaagctctcccc.....atcgtggaagcttattgtac 6000

Scoring table: IDENTITY NTC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5998.4	99.9	6000	10	ADJ94187
2	5976.8	99.6	37252	11	ACN44666 Human MYO
3	4888.8	81.5	6169	2	AAV51368 Human gen
4	4888.8	81.5	6169	3	AAAS7486 A TIGR (c
5	4069.4	67.8	5300	3	AAAS7484 A TIGR (c
6	4069.4	67.8	5300	12	ADFL13152 Human TIG
7	4069.4	67.8	5300	12	ADFL13152 Human tra
8	4068.4	67.8	5300	2	AAV51361 Human TIG
9	4067.8	67.8	5300	2	AAV51365 Human TIG
10	4067.8	67.8	5300	2	AAV51367 Human TIG
11	4067.8	67.8	5300	2	AAV51363 Human TIG
12	4067.8	67.8	5300	2	AAV51366 Human TIG
13	4067.8	67.8	5300	2	AAV51362 Human TIG
14	4065.4	67.6	5304	3	AAV51364 Human TIG
15	4057.4	66.9	5271	3	AAAS7485 A TIGR (c
16	4015.8	46.2	2800	3	AAAS7511 A TIGR (c
17	2773.4	46.2	2800	3	AAZ37968 Human GLC
18	2773.4	46.2	2800	11	ADL99152 Trabecula
19	2773.4	46.2	2800	14	ADZ67355 Human TIG

20	1382.2	23.0	3493	2	AAV37618	AAV37618 Human gla
21	1068.8	17.8	1086	8	ACA64937	ACA64937 Human GLC
22	1068.8	17.8	1086	12	ADO18110	Ado18110 Human sof
23	681.4	11.4	2117	8	ABZ58478	Abz58478 Human myo
24	681.4	11.4	2117	8	ABX10137	Abx10137 Human cdn
25	677.8	11.3	2145	4	AAAS15366	AAAS15366 CDNA enco
26	668.4	11.1	2082	11	ACN44667	Acn44667 Human mbrn
27	664.4	11.1	2115	12	ADO22683	Ado22683 Human sof
28	641.4	10.7	2031	4	AAD08141	Aad08141 Human tra
29	640.4	10.7	1548	2	AAV51391	AAV51391 Human TIG
30	640.4	10.7	1548	3	AAAS7509	AAAS7509 CDNA enco
31	640.4	10.7	1890	2	AAAS7606	AAAS7606 Human TIG
32	640.4	10.7	1939	2	AAV08904	AAV08904 TIGR prot
33	640.4	10.7	1939	2	AAV81910	AAV81910 Human tra
34	640.4	10.7	1939	5	AAAC87528	AAAC87528 Human TIG
35	640.4	10.7	2000	2	AAV33484	AAV33484 Trabecula
36	626.4	10.4	2061	9	ACH03575	ACH03575 CDNA enco
37	618	10.3	30057	11	ACN44664	Acn44664 Mouse gen
38	608	10.1	2800	3	AAZ37971	AAZ37971 Mouse gen
39	604.4	10.1	1512	2	AAV08905	AAV08905 TIGR prot
40	604.4	10.1	1512	5	AAAC87529	AAAC87529 Human TIG
41	604.4	10.1	1515	3	AAZ37974	AAZ37974 Human GLC
42	604.4	10.1	1515	8	ABX10138	Abx10138 Human TIG
43	604	10.1	604	12	ACH91949	ACH91949 Human gen
44	603.4	10.1	1512	2	AAV37619	AAV37619 Human gla
45	556.6	9.3	1969	2	AAZ30152	Aaz30152 Trabecula

## ALIGNMENTS

## RESULT 1

ADJ94187  
ID ADJ94187 strand: DNA, 6000 BP.

ADJ94187;  
AC ADJ94187;

DT 06-MAY-2004 (first entry)

DE Human MYOC gene in which glaucoma-inducing mutations are detected.

XX ds; glaucoma; detection; mutation; MYOC.

XX Homo sapiens.

XX WO2003083108-A1.

XX 09-OCT-2003.

XX 19-MAR-2003; 2003WO-JP003307.

XX 29-MAR-2002; 2002JP-00093443.

XX (SYSM-) SYSMEX CORP.

XX Asano K, Takahata T, Numada S, Masago A, Kouchi Y;

XX WPI; 2003-804059/75.

PT Examining genes to assess the risk of the onset of glaucoma by detecting mutations in the MYOC gene or the region upstream from it.

PS Claim 3; SEQ ID NO 1, 42pp; Japanese.

CC The invention relates to a method of examining genes to assess the risk of the onset of glaucoma comprising detection of at least two mutations in the glaucoma related gene encoding region and/or a region upstream from it. The glaucoma related gene is preferably the MYOC gene. The method is useful for the prevention or early detection of glaucoma. This sequence corresponds to the MYOC gene in which mutations are detected.

XX Sequence 6000 BP, 1586 A; 1285 C; 1499 G; 1630 T; 0 U; 0 Other;

Query Match	99.9%	Score 5998.4;	DB 10;	Length 6000;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 5999;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

OY		GCTCAAGAAAGTCTCCCACTCTAGACTCTGCAATCAAGATGTTACAGCAAACTC	60
Db	1	GCTCAAGAAAGTCTCCCACTCTAGACTCTGCAATCAAGATGTTACAGCAAACTC	60
OY		CGTAGAGGTAGGGTCTGTGTCTTACACTGATGCTTACACTGAGCTCACTGC	120
Db	61	CGTAGAGGTAGGGTCTGTGTCTTACACTGATGCTTACACTGAGCTCACTGC	120
OY		AACTTCGCTCCCAAGTTCAAGCAATCTCTGTCAAGCTCCCGGTAGCTGGAACT	180
Db	121	AACTTCGCTCCCAAGTTCAAGCAATCTCTGTCAAGCTCCCGGTAGCTGGAACT	180
OY		ACAGGCGCACGCCCGGCTAAATTTTGTATTGTATGATAGATGAGGGTTTCAATATTAG	240
Db	181	ACAGGCGCACGCCCGGCTAAATTTTGTATTGTATGATAGATGAGGGTTTCAATATTAG	240
OY		CCCGGCTGTCTTGAACCTCTGACCTCAGGTATCAACCCTCAAGCTCTTAAAGTGC	300
Db	241	CCCGGCTGTCTTGAACCTCTGACCTCAGGTATCAACCCTCAAGCTCTTAAAGTGC	300
OY		TGGGATTACAGGCAATGATCAACCGGCCCGGCGCAAGGTCAGTGTATTATTAAGAAATAC	360
Db	301	TGGGATTACAGGCAATGATCAACCGGCCCGGCGCAAGGTCAGTGTATTATTAAGAAATAC	360
OY		TTGAATGTTTACTAACAACCAAGGAAACAGCAAAAGCTGTGATATTTCAAGGATTC	420
Db	361	TTGAATGTTTACTAACAACCAAGGAAACAGCAAAAGCTGTGATATTTCAAGGATTC	420
OY		TTGGGATGAGGGAATGTGTCCATGAGCTGCTGCTATGTCAGACACACTGTGCTCATCA	480
Db	421	TTGGGATGAGGGAATGTGTCCATGAGCTGCTGCTATGTCAGACACACTGTGCTCATCA	480
OY		CTTTCTTCCCTCATCTCATTTTCAGGCTAAGTATCAATTTATTCACATGCTTTGTG	540
Db	481	CTTTCTTCCCTCATCTCATTTTCAGGCTAAGTATCAATTTATTCACATGCTTTGTG	540
OY		GTAAAGCTTCCACATGTTACTGAAATTAAGATATACATTAACATGATTCATTTGGAGCA	600
Db	541	GTAAAGCTTCCACATGTTACTGAAATTAAGATATACATTAACATGATTCATTTGGAGCA	600
OY		TCTGTGTGTGTATTAAGGGGAGAGGGGATACCCAGAGACTCCTTGAAGCCCCGGAG	660
Db	601	TCTGTGTGTGTATTAAGGGGAGAGGGGATACCCAGAGACTCCTTGAAGCCCCGGAG	660
OY		AGTGTTCCTCTCAAGCTGGGGGAGCCCTGCAAGCAACCGGGGATCTGTGGTGTCTGAGCA	720
Db	661	AGTGTTCCTCTCAAGCTGGGGGAGCCCTGCAAGCAACCGGGGATCTGTGGTGTCTGAGCA	720
OY		ACCTGCCAGCCCGTGCACCTGGTGTATTGTATCATCTCTAGGGAACCTGTGCTTCT	780
Db	721	ACCTGCCAGCCCGTGCACCTGGTGTATTGTATCATCTCTAGGGAACCTGTGCTTCT	780
OY		ATTTCGTGTGATCTCGTTCATTCATCCAGGATTCATGACAAATTATGATGATCTATA	840
Db	781	ATTTCGTGTGATCTCGTTCATTCATCCAGGATTCATGACAAATTATGATGATCTATA	840
OY		TCTGCACAGCACACAGAGCAAAATGTGTAGCAAAAGCACTGCTACCTTGTGTGAG	900
Db	841	TCTGCACAGCACACAGAGCAAAATGTGTAGCAAAAGCACTGCTACCTTGTGTGAG	900
OY		GTTGACAGTTTCTCANGAAGAGTGTGAGAAAGAAATTAATAGCCGCACTTAAACCA	960
Db	901	GTTGACAGTTTCTCANGAAGAGTGTGAGAAAGAAATTAATAGCCGCACTTAAACCA	960
OY		GTGCTGAAGAAAGAAATTAACACCATCTTGAAGAAATTGTGCGCAGCATCCCTTAAACA	1020
Db	961	GTGCTGAAGAAAGAAATTAACACCATCTTGAAGAAATTGTGCGCAGCATCCCTTAAACA	1020
OY		GAGCACCTTCAGCGCCCTGCTGCTCCATCGTGTGCCCGGAGGCCCCCAAGCCGAGT	1080

Db	1021	GGCCACCTCCCTACGGCCCCCTGGCTGCATGTGCCCCGGAGGCCCCCAAGCCGAGT	1080
Qy	1081	CTTCCAAAGCCTCTCTCCATCACTCAACAGGCTGCAAGCTGAGCTGCTGCTTCCCGTG	1140
Db	1081	CTTCCAAAGCCTCTCTCCATCACTCAACAGGCTGCAAGCTGAGCTGAGCTGCTGCTTCCCGTG	1140
Qy	1141	AAATGTCCTGGTGAATCTGAGCTGGAGACTCTTGGCCCAAGGCTCCAGAAAGGAAATG	1200
Db	1141	AAATGTCCTGGTGAATCTGAGCTGGAGACTCTTGGCTCCAGAGCTCCAGAAAGGAAATG	1200
Qy	1201	AGAGGAAAACTAAGCTTAAACGAGATCTGAGAGGAGAGTGTTCCTCAGAGGAAAAGG	1260
Db	1201	AGAGGAAAACTAAGCTTAAACGAGAAATCTGAGAGGAGAGTGTTCCTCAGAGGAAAAGG	1260
Qy	1261	GCCTCCAGTCCAGAGAAATTCAGAGAGTGGGACTGCAAGGAGTGGGAGCGCTGGGC	1320
Db	1261	GCCTCCAGTCCAGAGAAATTCAGAGAGTGGGAGTCCAGAGGAGTGGGAGCGCTGGGC	1320
Qy	1321	TGAGCGGGTCTGAAAGGCAAGAGGTGAAAGGCAAGGCTGAAGCTGCCAATGTC	1380
Db	1321	TGAGCGGGTCTGAAAGGCAAGAGGTGAAAGGCAAGGCTGAAGCTGCCAATGTC	1380
Qy	1381	AGTGTGTTCAAGGGGCTGGGAGTTCCTCCGTGCTCCTGTGACCTTTTATCTTCTCT	1440
Db	1381	AGTGTGTTCAAGGGGCTGGGAGTTCCTCCGTGCTCCTGTGACCTTTTATCTTCTCT	1440
Qy	1441	CTGCTGGAGAGAAAGTCTAATTTCAAGAGGATGCACTTTCATTAAGTCAAGCTGT	1500
Db	1441	CTGCTGGAGAGAAAGTCTAATTTCAAGAGGATGCACTTTCATTAAGTCAAGCTGT	1500
Qy	1501	AAATTCAGAGGTGTGCAATGGGTTTTCTTCAAGAGGCTTTTATTTAATGGAAATAG	1560
Db	1501	AAATTCAGAGGTGTGCAATGGGTTTTCTTCAAGAGGCTTTTATTTAATGGAAATAG	1560
Qy	1561	GAGCGAGCTCATTTCCTAGGCGGTAAATTCAGGAAAGATGACTGAGTCTTCTCTT	1620
Db	1561	GAGCGAGCTCATTTCCTAGGCGGTAAATTCAGGAAAGATGACTGAGTCTTCTCTT	1620
Qy	1621	CATGCTTCTGGGCACTACTCAAGCCCTGTGTGATCTTGGCTTAATGCAAGCGTTCGA	1680
Db	1621	CATGCTTCTGGGCACTACTCAAGCCCTGTGTGATCTTGGCTTAATGCAAGCGTTCGA	1680
Qy	1681	AACTTGGAAATCAGAGACTCGAGTTTCTTGTGCTTGTGCAATGTGTGCTGTGCAC	1740
Db	1681	AACTTGGAAATCAGAGACTCGAGTTTCTTGTGCTTGTGCAATGTGTGCTGTGCAC	1740
Qy	1741	CGTGGCAAGTGTCTCTCCCTCCGGGCAATAGCTTCTGTGCTAATAAGCCTTGCA	1800
Db	1741	CGTGGCAAGTGTCTCTCCCTCCGGGCAATAGCTTCTGTGCTAATAAGCCTTGCA	1800
Qy	1801	GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTGTGTGAGGGGAGTGTGAGAGGG	1860
Db	1801	GCTCTCGTGTCTGTGAACCTTCCCTGTGATTCCTGTGTGAGGGGAGTGTGAGAGGG	1860
Qy	1861	AAGAGGAGAGCTGGAGCACTGAGCCAGGCAAGGGAGGTGAGAGGGGCAAGAGGCAAG	1920
Db	1861	AAGAGGAGAGCTGGAGCACTGAGCCAGGCAAGGGAGGTGAGAGGGGCAAGAGGCAAG	1920
Qy	1921	CAGAAAGCTGGGTGTCTCAATGCTCTCACTGATCACTGATCACTCAAGACCGAAGGCA	1980
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Qy	1981	CAATGCTCAGGAAAGCTCAATGAACCAAGCAAGCCATTTTCTTCCCTAAGCATAGAC	2040
Db	1981	CAATGCTCAGGAAAGCTCAATGAACCAAGCAAGCCATTTTCTTCCCTAAGCATAGAC	2040
Qy	2041	AATGGCATTTGGCAATTAACAAAAGATGCAAGACTTAATGAGTGTAGCTTTTGGCTG	2100
Db	2041	AATGGCATTTGGCAATTAACAAAAGATGCAAGACTTAATGAGTGTAGCTTTTGGCTG	2100
Qy	2101	GCATTCAAAAACCTGGCCAGAGCAATGGAATATGCCAGAAATTTTAACTTTCAACC	2160
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Db 5341 CTGGTCCCTTTGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5400
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RESULT 2
ACN44666
ID ACN44666 standard; DNA; 37252 BP.
XX
AC ACN44666;
XX
AC 18-NOV-2004 (first entry)
XX
DE Human genomic sequence hCG37091.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR MPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 1228; Opp; English.
XX

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CC The present invention relates to novel DNA and protein sequences which  
 CC are associated with carcinomas. The sequences are useful for: (i) for  
 CC screening drug candidates; (ii) for screening of bioactive agent capable  
 CC of binding to Carcino Associated Protein (CAP); (iii) for screening of  
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;  
 CC for diagnosing carcinoma or a propensity to carcinoma; and (x) for  
 CC determining Carcino Associated (CA) gene copy number. In addition, the  
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
 CC carcinoma including lymphoma. The present sequence is one such CA coding  
 CC sequence. Note: This patent is an equivalent to basic patent  
 CC US2002182586A1, for which no sequence data was published  
 CC XX

Sequence 37252 BP; 10006 A; 8724 C; 8201 G; 10321 T; 0 U; 0 Other;

Query Match 99.6%; Score 5976.8; DB 11; Length 37252;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5993; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 GCTCCAGAGAACTCCCACTCTGACTTCTGACATCAGATGTTACAGCCAGAACTC 60  
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 DB 6066 AACCTCTGCTCCCAAGTTCAAGCAATCTCTGTCTCAGCCCTCCGCGTGGAGACT 6125  
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RESULT 3  
 AAV51368  
 ID AAV51368 standard; DNA, 6169 BP.  
 XX AAV51368;  
 AC XX  
 AC XX  
 DT 27-OCT-1998 (first entry)  
 XX XX  
 DE Human TIGR upstream region and exon 1 DNA.  
 XX TIGR; trabecular meshwork induced glucocorticoid response protein; human;  
 KW diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
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XX FT /*tag= b
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XX FT /*tag= c
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XX FT /note= "partial intron sequence"
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XX PD 30-JUL-1998.
XX PR 09-JAN-1998; 98MO-US000468.
XX PR 28-JAN-1997; 97US-00791154.
XX PR 26-SEP-1997; 97US-00938669.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Nguyen TD, Polansky JR, Chen P, Chen H;
XX DR WPI; 1998-427946/36.
XX PT Use of TIGR nucleic acid sequences - used for, e.g. developing products
XX PS for diagnosis, prognosis and treatment of glaucoma.
XX PS Claim 37; Fig 3; 105pp; English.
XX CC This sequence is a trabecular meshwork induced glucocorticoid response
XX CC protein (TIGR) upstream region and exon 1. This DNA sequence can be used
XX CC in a method for diagnosing glaucoma in a patient. The method involves the
XX CC detection of polymorphisms whose presence is predictive of a mutation
XX CC affecting TIGR response in the patient and can be diagnostic of glaucoma
XX CC or steroid sensitivity. Base substitutions and base additions upstream of
XX CC and within TIGR exons can also be used to diagnose glaucoma
SQ Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;
Query Match 81.5%; Score 4888.8; DB 2; Length 6169;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;
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DB 1276 CGTGAAGGTGAGGTCTGTGTCTTACACCTAGCTGATGCTTACACCTGAGCTCACTGC 1335
QY 121 AACCTGTGCTCCAGGTCAAGCAATCTCTGTCTCAGCCTCCGCGTAGCTGGACT 180
DB 1336 AACCTGTGCTCCAGGTCAAGCAATCTCTGTCTCAGCCTCCGCGTAGCTGGACT 1395
QY 181 AAGAGGCGACGCCCGCTAATTTTGTATTGTTAGTAGAGATGGGTTTACCATATTAG 240
DB 1396 AAGAGGCGACGCCCGCTAATTTTGTATTGTTAGTAGAGATGGGTTTACCATATTAG 1455
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DB 1516 TGGGATTACAGGATGATCAGCGCGCCGCGCAAGAGGTCAAGTGTTTAATAAGAAATAAC 1575

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DB |||||  
DB 3136 CAGAACTGGGTGCTCATCTAGTCCCTCATCTGATCTGTCAGACTCCAGGACCGAAGCCCA 3195  
QY 1981 CAATGCTTCAGAAAGCTCAATGAACCCAAACAGCCACATTTTCTTCCCTTAAGCATAGAC 2040  
DB |||||  
DB 3196 CAATGCTTCAGAAAGCTCAATGAACCCAAACAGCCACATTTTCTTCCCTTAAGCATAGAC 3255  
QY 2041 AATGCAATTTGCGAATTAACCAAAAAGATGCAAGACTAATCTGTGTGTAGCTTTTGCTGT 2100  
DB |||||  
DB 3256 AATGCAATTTGCGAATTAACCAAAAAGATGCAAGACTAATCTGTGTGTAGCTTTTGCTGT 3315  
QY 2101 GCATTCAAAACATCGGGCCAGAGCAAGTGAATAATGCGAGATGTGTAACCTTTTCAACC 2160  
DB |||||  
DB 3316 GCATTCAAAACATCGGGCCAGAGCAAGTGAATAATGCGAGATGTGTAACCTTTTCAACC 3375  
QY 2161 TGACCAAGCACCCCAACGAGCTGAGAGTGTGCTGACAGACAGAGTGAACCTGAGCGC 2220  
DB |||||  
DB 3376 TGACCAAGCACCCCAACGAGCTGAGAGTGTGCTGACAGACAGAGTGAACCTGAGCGC 3435  
QY 2221 AAGGGAGGAGAAAGAAAGAGGGATGTATATGACAAAGAAACAGATTCATTCAAG 2280  
DB |||||  
DB 3436 AAGGGAGGAGAAAGAAAGAGGGATGTATATGACAAAGAAACAGATTCATTCAAG 3495  
QY 2281 GGCAGTGGGAATTTGACACAGGGATTTATAGTCAAGTATCTCGGGTCTAGAGAGCGAG 2340  
DB |||||  
DB 3496 GGCAGTGGGAATTTGACACAGGGATTTATAGTCAAGTATCTCGGGTCTAGAGAGCGAG 3555  
QY 2341 GCTATATTTGTGGGGGAAAAATCAATTCAAGGGAAGTGGGAGACTGATTTTCTAATAC 2400  
DB |||||  
DB 3556 GCTATATTTGTGGGGGAAAAATCAATTCAAGGGAAGTGGGAGACTGATTTTCTAATAC 3615  
QY 2401 TATATTTTCTCTTACAGCTGATATTTCTGAGCAAGTCAAGATGTAACTGAGGCT 2460  
DB |||||  
DB 3616 TATATTTTCTCTTACAGCTGATATTTCTGAGCAAGTCAAGATGTAACTGAGGCT 3675  
QY 2461 GTAAGATTAAGTATTTCTCTTATTAAGAACTTTTCTGTGTGAGTTAGCAGACA 2520  
DB |||||  
DB 3676 GTAAGATTAAGTATTTCTCTTATTAAGAACTTTTCTGTGTGAGTTAGCAGACA 3735  
QY 2521 AGGGCAATCCCGTTTCTTTTAAACAGAAAGAAAAATTCCTTAAGATTAAGCCAAACAGAT 2580

DB 3736 AGGGCAATCCCGTTTCTTTTAAACAGAAAGAAAAATTCCTTAAGATTAAGCCAAACAGAT 3795  
QY 2581 TCAAGCTTAAGTCTTGCTGACTATATATGATGTGTTTTTGAATAATCATTTCCAGCATGTT 2640  
DB |||||  
DB 3796 TCAAGCTTAAGTCTTGCTGACTATATATGATGTGTTTTTGAATAATAATCATTTCCAGCATGTT 3855  
QY 2641 TACTATCTGATTCAAGAAATGAGACTATATCCCTTGGTGCAGCTGTAAACAAACCCAT 2700  
DB |||||  
DB 3856 TACTATCTGATTCAAGAAATGAGACTATATCCCTTGGTGCAGCTGTAAACAAACCCAG 3915  
QY 2701 TTTGAATATGTCGAAGTTCAAGCTTAACTGAGAAACCAATCAATATAGAAATGAAATCTTT 2760  
DB |||||  
DB 3916 TTTGAATATGTCGAAGTTCAAGCTTAACTGAGAAACCAATCAAAAGAAATGAAATCTTT 3974  
QY 2761 AGAGCAAACTGTGTTTCTCCAC-TTGAAGGTGAGTCTGCCAGGGCAGTTTGGAAATATT 2819  
DB |||||  
DB 3975 AGAGCAAACTGTGTTTCTCCACATCTGAGAGGTGAGTGCAGGGCAGTTTGGAAATATT 4034  
QY 2820 TACTTCAAGATTAATGACATGTGTGTGTAATTAACAATTAAGTGTCTCAAGGCAAT 2879  
DB |||||  
DB 4035 TACTTCAAGATTAATGACATGTGTGTGTAATTAACAATTAAGTGTCTCAAGGCAAT 4094  
QY 2880 CATTAATTTCAAGTGGCTTAAAGTTACTCTGACAGTTTGGTATATTTATTTGGCTATTGTC 2939  
DB |||||  
DB 4095 CATTAATTTCAAGTGGCTTAAAGTTACTCTGACAGTTTGGTATATTTATTTGGCTATTGTC 4154  
QY 2940 CATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTTTAACCTA 2999  
DB |||||  
DB 4155 CATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAAGCAGGATTTTAACCTA 4214  
QY 3000 CAGTCCAGAAAGCCGTGAAATTTGAATGAGAAAAATTAACATTTTGTGTTTACCACT 3059  
DB |||||  
DB 4215 CAGTCCAGAAAGCCGTGAAATTTGAATGAGAAAAATTAACATTTTGTGTTTACCACT 4274  
QY 3060 TCTAATTAATTTTAAACATTTTATTTCAATGCGAAATGAGCCATTAACCTCAAGTGGTAT 3119  
DB |||||  
DB 4275 TCTAATTAATTTTAAACATTTTATTTCAATGCGAAATGAGCCATTAACCTCAAGTGGTAT 4334  
QY 3120 AACGATACCTGTGATTTTGTCAATTAACAAATGAATCAAGACATTTTATATCTAATATTAC 3179  
DB |||||  
DB 4335 AACGATACCTGTGATTTTGTCAATTAACAAATGAATCAAGACATTTTATATCTAATATTAC 4394  
QY 3180 AGTTGTGCAGATACGTTGTATGGAATAATTTATACCAAAACATCTTTGAAATTAAC 3239  
DB |||||  
DB 4395 AGTTGTGCAGATACGTTGTATGGAATAATTTATACCAAAACATCTTTGAAATTAAC 4454  
QY 3240 CTCCTGTGATCTTGTGTTTTTAAATTAATTAACATGTTTAAATTTGATATTG 3299  
DB |||||  
DB 4455 CTCCTGTGATCTTGTGTTTTTAAATTAATTAACATGTTTAAATTTGATATTG 4514  
QY 3300 AATATCATATTTCAATATCAATTTGTTTCTTTGTATATCTAATATTTATATTTGAAATAC 3359  
DB |||||  
DB 4515 AATATCATATTTCAATATCAATTTGTTTCTTTGTATATCTAATATTTATATTTGAAATAC 4574  
QY 3360 AATCTTTCGAAAGAGTTCCCAAGATTTTCAACAAATGAGCTCTTGGAATGACACACA 3419  
DB |||||  
DB 4575 AATCTTTCGAAAGAGTTCCCAAGATTTTCAACAAATGAGCTCTTGGAATGACACACA 4634  
QY 3420 GAGTAAAGACTGATTTAGAGGCTAAATTTGCAATTTGGTCCCTGAGATGCAAGACTGAAT 3479  
DB |||||  
DB 4635 GAGTAAAGACTGATTTAGAGGCTAAATTTGCAATTTGGTCCCTGAGATGCAAGACTGAAT 4694  
QY 3480 TAGAAAGTTCTCCCAAGATTAACAAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAAATCTG 3539  
DB |||||  
DB 4695 TAGAAAGTTCTCCCAAGATTAACAAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAAATCTG 4754  
QY 3540 CCGCTCTATATGAAATGCTCCCTGAGAGCTGTATAGGGTGTGCTGTGCTCTGCT 3599  
DB |||||  
DB 4755 CCGCTCTATATGAAATGCTCCCTGAGAGCTGTATAGGGTGTGCTGTGCTCTGCT 4814  
QY 3600 GGTGTATATTTTCTGTCTCCCTGTACGTTTAAAGAACTTGTGGAATCTCCAGTTTCC 3659  
DB |||||





CC glucocorticoid receptor) promoter. The specification describes a method  
CC for the diagnosis, prognosis and treatment of glaucoma, based on  
CC detecting specific polymorphisms in the promoter of the TIGR gene. The  
CC method is used for diagnosis and prognosis of glaucoma (of all types),  
CC steroid sensitivity and progressive ocular hypertension that leads to  
CC loss of vision. Glaucoma can be treated by administering an agent that  
CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter  
CC (or other regulatory regions) can be used to express homologous or  
CC heterologous genes, particularly for tissue-specific expression of  
CC therapeutic transgenes for treating glaucoma, also to generate transgenic  
CC animals and in screening for compounds (specific modulators) with  
CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can  
CC be used as amplification primers or probes, e.g. for isolating related  
CC sequences in non-human animals  
XX

Sequence 6169 BP; 1702 A; 1389 C; 1491 G; 1587 T; 0 U; 0 Other;

Query Match 81.5%; Score 4888.8; DB 3; Length 6169;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;

QY 1 GCTCCAGGAGTCTCCCACTCTGACTTTCGATCAGAGTTTACAGCCAGAACTC 60  
DB 1216 GCTCCAGGAGTCTCCCACTCTGACTTTCGATCAGAGTTTACAGCCAGAACTC 1275  
QY 61 CGTGAAGGTGAGGGTCTGTGTCTTACACCTATGCTCTACACCTGAGCTCATG 120  
DB 1276 CGTGAAGGTGAGGGTCTGTGTCTTACACCTATGCTCTACACCTGAGCTCATG 1335  
QY 121 AACCTCTGCTCCAGAGTTTCAAGCAATCTCTGTCTCAGCCCTCCGCGTGGAGCT 180  
DB 1336 AACCTCTGCTCCAGAGTTTCAAGCAATCTCTGTCTCAGCCCTCCGCGTGGAGCT 1395  
QY 181 AAGAGGGCAGCGCCGCTAATTTTGTATTTAGTATGAGATGGGTTTCAACATTTAG 240  
DB 1396 AAGAGGGCAGCGCCGCTAATTTTGTATTTAGTATGAGATGGGTTTCAACATTTAG 1455  
QY 241 CCGCGTGGTCTTGAATCTCCAGCTCAGGTGATCCAGCCCTCCTAAAGTG 300  
DB 1456 CCGCGTGGTCTTGAATCTCCAGCTCAGGTGATCCAGCCCTCCTAAAGTG 1515  
QY 301 TGGGATTAAGAGATGATCAGCGCGCCGCGCAAGGTTCAAGTTTAAAGAAATAAC 360  
DB 1516 TGGGATTAAGAGATGATCAGCGCGCCGCGCAAGGTTCAAGTTTAAAGAAATAAC 1575  
QY 361 TTGAATGTTTACTAAACCAAGGAAACAGCAAAAGCTGATTAATTTCAAGGATTC 420  
DB 1576 TTGAATGTTTACTAAACCAAGGAAACAGCAAAAGCTGATTAATTTCAAGGATTC 1635  
QY 421 TTGGGATGGGGAATGGTGCATGAGCTGCTGCTAGTCCAGACACTGCTCTCATCA 480  
DB 1636 TTGGGATGGGGAATGGTGCATGAGCTGCTGCTAGTCCAGACACTGCTCTCATCA 1695  
QY 481 GTTCTTCTCCTCATCTCAATTTTCAAGGCTAAGTTTACATTTTATTCACCATGTTTGTG 540  
DB 1696 GTTCTTCTCCTCATCTCAATTTTCAAGGCTAAGTTTACATTTTATTCACCATGTTTGTG 1755  
QY 541 GTTAAGCTTCATCGTTACTGAATTAAGATATACATTAACCTAGTTTCAATTTGGGGCCA 600  
DB 1756 GTTAAGCTTCATCGTTACTGAATTAAGATATACATTAACCTAGTTTCAATTTGGGGCCA 1815  
QY 601 TCTGTGTGTGTATATGAGGAGAGGAGGCAATACCCAGAGACTCTTTGAAGCCCCCGGAG 660  
DB 1816 TCTGTGTGTGTATATGAGGAGAGGAGGCAATACCCAGAGACTCTTTGAAGCCCCCGGAG 1875  
QY 661 AAGTTTCTCTCTCAAGTGGGAGAGCCCTGCAAGCAACCCGCGGTCTTGAGTCTTGAAGA 720  
DB 1876 AAGTTTCTCTCTCAAGTGGGAGAGCCCTGCAAGCAACCCGCGGTCTTGAGTCTTGAAGA 1935  
QY 721 AACTGCAAGCCGCTGCACTGATTTTGTATATCACTCTTAAGGAGACTGTTGCTTTCT 780  
DB 1936 AACTGCAAGCCGCTGCACTGATTTTGTATATCACTCTTAAGGAGACTGTTGCTTTCT 1995

QY 781 ATTCTGTGTGACTCGTTCAATTCATCCAGGACTTTCATGCAATTTATGAGACTTATA 840  
DB 1996 ATTCTGTGTGACTCGTTCAATTCATCCAGGACTTTCATGCAATTTATGAGACTTATA 2055  
QY 841 TCTGCAGACACCAAGAGCAAAATGTTGAGCAAGAGCTCACTGCCCTACCTTGTGAG 900  
DB 2056 TCTGCAGACACCAAGAGCAAAATGTTGAGCAAGAGCTCACTGCCCTACCTTGTGAG 2115  
QY 901 GTGACAGTTTTCATAGAGAGAGTGTGAGAAAGAAATTAATAGCCACCACTTAAACCA 960  
DB 2116 GTGACAGTTTTCATAGAGAGAGTGTGAGAAAGAAATTAATAGCCACCACTTAAACCA 2175  
QY 961 GTGCTAAAGAAAGAAATTAACCACTTTGAAGATTTGTGGAGCAATCCCTTAACA 1020  
DB 2176 GTGCTAAAGAAAGAAATTAACCACTTTGAAGATTTGTGGAGCAATCCCTTAACA 2235  
QY 1021 GGCCACTTCCCTAGGCCCCCTGCTGCTCATATGTCGCCGAGGCCCAAGCCGAGT 1080  
DB 2236 GGCCACTTCCCTAGGCCCCCTGCTGCTCATATGTCGCCGAGGCCCAAGCCGAGT 2295  
QY 1081 CTTCCAGGCTCTCTCTCATATGATCAAGCCGTGACGCTGGCTGCTGCTCCGCTG 1140  
DB 2296 CTTCCAGGCTCTCTCTCATATGATCAAGCCGTGACGCTGGCTGCTGCTCCGCTG 2355  
QY 1141 AATCGTCTGTGATCTGAGGTGAGACTCTCTGCTCAGGCTCCAGAAAGAAATAG 1200  
DB 2356 AATCGTCTGTGATCTGAGGTGAGACTCTCTGCTCAGGCTCCAGAAAGAAATAG 2415  
QY 1201 AAGAGGAACTAGTCTAACGAGAAATCTGAGAGGAGCAGTGTCTCTCAGAGGAAAGG 1260  
DB 2416 AAGAGGAACTAGTCTAACGAGAAATCTGAGAGGAGCAGTGTCTCTCAGAGGAAAGG 2475  
QY 1261 GCTCTCAGCTCAGAGAAATTCAGAGGTGGGAGCTGCAAGGAGTGGGAGCGTGGGCT 1320  
DB 2476 GCTCTCAGCTCAGAGAAATTCAGAGGTGGGAGCTGCAAGGAGTGGGAGCGTGGGCT 2535  
QY 1321 TGAGCGGGGTGAGAAAGGAGAGGAGTGAAGAGGCAAGGCTGAGCTGCCAGATGTC 1380  
DB 2536 TGAGCGGGGTGAGAAAGGAGAGGAGTGAAGAGGCAAGGCTGAGCTGCCAGATGTC 2595  
QY 1381 AGTGTGTTTCAAGGAGCTGGAGATTTTCCGTGCTCTCTGTGAGCTTTTATCTTTCT 1440  
DB 2596 AGTGTGTTTCAAGGAGCTGGAGATTTTCCGTGCTCTCTGTGAGCTTTTATCTTTCT 2655  
QY 1441 CTGCTTGAAGAGAAAGAGTCTATTTCAATGAAGGATGCAATTTCAATTAAGCTGCT 1500  
DB 2656 CTGCTTGAAGAGAAAGAGTCTATTTCAATGAAGGATGCAATTTCAATTAAGCTGCT 2715  
QY 1501 AAAATTCAGAGGTGAGATGGGTTTCTCTCAAGAGGCTTTAATTAAGGAAATATAG 1560  
DB 2716 AAAATTCAGAGGTGAGATGGGTTTCTCTCAAGAGGCTTTAATTAAGGAAATATAG 2775  
QY 1561 GAAGGAGCTCATTTCTAGGCCCCGTTAATTCACGGAAGAGTCACTGAGTCTTTCTTT 1620  
DB 2776 GAAGGAGCTCATTTCTAGGCCCCGTTAATTCACGGAAGAGTCACTGAGTCTTTCTTT 2835  
QY 1621 CATGCTTCTGGGCACTACTCAAGCTGCTGAGTCACTTGGCTTATGCAAGCGTGCAG 1680  
DB 2836 CATGCTTCTGGGCACTACTCAAGCTGCTGAGTCACTTGGCTTATGCAAGCGTGCAG 2895  
QY 1681 AACCTTGAATCAGAGAGCTGGTTTCTTTCTGATTTGCAATTTGATGAGCTGTCAG 1740  
DB 2896 AACCTTGAATCAGAGAGCTGGTTTCTTTCTGATTTGCAATTTGATGAGCTGTCAG 2955  
QY 1741 CGTGGGCAAGTGTCTCTCTCTCCCTGAGGCAATAGCTCTCTGCTATTAAGACCTTGCA 1800  
DB 2956 CGTGGGCAAGTGTCTCTCTCTCCCTGAGGCAATAGCTCTCTGCTATTAAGACCTTGCA 3015  
QY 1801 GCTCTGCTGTTCTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAGAGGG 1860  
DB 3016 GCTCTGCTGTTCTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAGAGGG 3075  
QY 1861 AAGAGGAGAGCTGAGCAAGCTGAGCAAGGGGAGTGAAGGGGAGCAAGAAAGCAGG 1920

Db	3076	AAAGAGGAGAGCTGGAGACAGCTGAGCCAGAGGGAGTGAAGGGAGACAGAAAGGACAGG	3135
Qy	1921	CAGAAAGCTGGGTGCTCCATCAAGTCCCTCACTGATCAGCTCAAGCTCCAGAACCGAGAGCCA	1980
Db	3136	CAGAAAGCTGGGTGCTCCATCAAGTCCCTCACTGATCAGCTCAAGCTCCAGAACCGAGAGCCA	3195
Qy	1981	CAATGCTTCAGGAAAGCTCAATGAACCAACAGCACATTTTCCTTCCCTTAAGCATAGAC	2040
Db	3196	CAATGCTTCAGGAAAGCTCAATGAACCAACAGCACATTTTCCTTCCCTTAAGCATAGAC	3255
Qy	2041	AAATGGCAATTTGGCAATTAACCAAAAAGATGAGAGCATAACTGGTGTAGCTTTTGCTG	2100
Db	3356	AATGGCAATTTGGCAATTAACCAAAAAGATGAGAGCATAACTGGTGTAGCTTTTGCTG	3315
Qy	2101	GCATTCCAAAACTGGGCGACAGCAAGTGGAAAAATGACAGAGATTGTTAACTTTTCACC	2160
Db	3316	GCATTCCAAAACTGGGCGACAGCAAGTGGAAAAATGACAGAGATTGTTAACTTTTCACC	3375
Qy	2161	TGACCAAGACCCCAAGCAGCTCAGCAGTGACTGCTGACAGCAAGAGTGAACCTGACAGC	2220
Db	3376	TGACCAAGACCCCAAGCAGCTCAGCAGTGACTGCTGACAGCAAGAGTGAACCTGACAGC	3435
Qy	2221	AGGGAGAGAGAAAAAGAGAGGATAGTCTTAGACCAAGAAAGACAGATTCACTTCAAG	2280
Db	3436	AGGGAGAGAGAAAAAGAGAGGATAGTCTTAGACCAAGAAAGACAGATTCACTTCAAG	3495
Qy	2281	GGCAGTGGGAATTTGACCAAGAGATTATAGTCCAGCTGATCCTGGGTTCTAGAGAGCAGG	2340
Db	3496	GGCAGTGGGAATTTGACCAAGAGATTATAGTCCAGCTGATCCTGGGTTCTAGAGAGCAGG	3555
Qy	2341	GCTATATTTGTGGGGGAAAAAATCATGTTCAAGGAAAGTCGGGAGACTGATTTCTAATAC	2400
Db	3556	GCTATATTTGTGGGGGAAAAAATCATGTTCAAGGAAAGTCGGGAGACTGATTTCTAATAC	3615
Qy	2401	TATATTTTTCCTTTACAAGCTGAGTAATTTGACCAAGTCAACAAGTATAGTAATGAGGCT	2460
Db	3616	TATATTTTTCCTTTACAAGCTGAGTAATTTGACCAAGTCAACAAGTATAGTAATGAGGCT	3675
Qy	2461	GTAAGATTACTTAGTTTCCTCTTATTAGGAACCTCTTTTCTCTGGAGTTAGACAGACA	2520
Db	3676	GTAAGATTACTTAGTTTCCTCTTATTAGGAACCTCTTTTCTCTGGAGTTAGACAGACA	3735
Qy	2521	AGGGCAATCCCGTTTCCTTTACAAGAAAGAAAACTTCTAAGATAAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTTCCTTTACAAGAAAGAAAACTTCTAAGATAAAGCCAAACAGAT	3795
Qy	2581	TCAAGCCTAAGCTCTTGCTGACTATATGATTTGGTTTTGAAAAATCATTTCAAGGATGTT	2640
Db	3796	TCAAGCCTAAGCTCTTGCTGACTATATGATTTGGTTTTGAAAAATCATTTCAAGGATGTT	3855
Qy	2641	TACTATCTGATTCAAGAAATGAGACTAGAGACCCTTGGTCAAGCTGTAAACAAACCCCAT	2700
Db	3856	TACTATCTGATTCAAGAAATGAGACTAGAGACCCTTGGTCAAGCTGTAAACAAACCCCAT	3915
Qy	2701	TTGTAAATGTCTCAAGTTCAAGCTTAACCTGCAAGAACCAATCAATTAAGATAGAACTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAAGCTTAACCTGCAAGAACCAATCAATTAAGATAGAACTTT	3974
Qy	2761	AAGCAAACTGTGTTTCTTCAC-TCTGAGGTGAGTCTGCCAGGCACTTTGGAAATATT	2819
Db	3975	AAGCAAACTGTGTTTCTTCAC-TCTGAGGTGAGTCTGCCAGGCACTTTGGAAATATT	4034
Qy	2820	TACTTCAAAAGTATGACCTGTGTGGTATTAACAATTAAGTTGCTCAAAAGGCAT	2879
Db	4035	TACTTCAAAAGTATGACCTGTGTGGTATTAACAATTAAGTTGCTCAAAAGGCAT	4094
Qy	2880	CATTATTTCAAGTGGCTTAAGATTCTTGAACGTTTGGTATATTTATGGCTATTGC	2939
Db	4095	CATTATTTCAAGTGGCTTAAGATTCTTGAACGTTTGGTATATTTATGGCTATTGC	4154
Qy	2940	CATTGCTTTTGTGTTTTCTCTTGGGTTTATATATGAAGCAGGATTTATTAACCTA	2999

Db	4155	CATTGCTTTTGGTTTTTTCCTTGGGTATTAATGTAAGACAGGATTAATAACCTA	4214
Qy	3000	CAGTCCAGAAAGCCTGTGAATTGAATGAGAAAAAATTAATCTTTTGTTTTAAACCACT	3059
Db	4215	CAGTCCAGAAAGCCTGTGAATTGAATGAGAAAAAATTAATCAATTTTGTTTTAAACCACT	4274
Qy	3060	TCCTAACCTAAATTTTAACTTTTATCTCAATGGGAATAGAGCACTAACTCAAGAGGTAAAT	3119
Db	4275	TCCTAACCTAAATTTTAACTTTTATCTCAATGGGAATAGAGCACTAACTCAAGAGGTAAAT	4334
Qy	3120	AACAGTACCTGTGATTTTGTTCATTTACCAATAGAAATCAGACATTTTATTAATTAATAC	3179
Db	4335	AACAGTACCTGTGATTTTGTTCATTTACCAATAGAAATCAGACATTTTATTAATTAATAC	4394
Qy	3180	AGTTGTGCAGATACGTTGTAGTGAATATTTATCTCAAACTACTTTGAAATTTAGC	3239
Db	4395	AGTTGTGCAGATACGTTGTAGTGAATATTTATCTCAAACTACTTTGAAATTTAGC	4454
Qy	3240	CTCCGTGCGAATCTGTGTTTTTAACTAATTAATAAATGTTTAAATTTTGAATTTTG	3299
Db	4455	CTCCGTGCGAATCTGTGTTTTTAACTAATTAATAAATGTTTAAATTTTGAATTTTG	4514
Qy	3300	ATAATCATATTTCTAATTAATCAATTTGTTTCCTTTGTAACTAATATTTTAAATTTGAAAC	3359
Db	4515	ATAATCATATTTCTAATTAATCAATTTGTTTCCTTTGTAACTAATATTTTAAATTTGAAAC	4574
Qy	3360	ATCTTCTGAGAAAGTCCCAAGATTTTACCAATGAGGTTCTTGAGTACACACACA	3419
Db	4575	ATCTTCTGAGAAAGTCCCAAGATTTTACCAATGAGGTTCTTGAGTACACACACA	4634
Qy	3420	GAGTAAAGACGTATTTAGAGGCTTAACTATGACATTTGGTCTGATGATGCAAGACTGAAT	3479
Db	4635	GAGTAAAGACGTATTTAGAGGCTTAACTATGACATTTGGTCTGATGATGCAAGACTGAAT	4694
Qy	3480	TAGAAAGTCTCCCAAGATACACAGTGTTTTAAAGCTAGAGGCTGAAGGGGAAATCTG	3539
Db	4695	TAGAAAGTCTCCCAAGATACACAGTGTTTTAAAGCTAGAGGCTGAAGGGGAAATCTG	4754
Qy	3540	CCGCTTCTAATAGAAATGCTCTTCCCTGAGACCTGTAAGGCTGTCTTGTGTTCTGGCT	3599
Db	4755	CCGCTTCTAATAGAAATGCTCTTCCCTGAGACCTGTAAGGCTGTCTTGTGTTCTGGCT	4814
Qy	3600	GAGCTGTATTTTCTGTCTTCCCTGCTAAGTCTTAAAGACTTTGTTTGAATCTCCAGTTCC	3659
Db	4815	GAGCTGTATTTTCTGTCTTCCCTGCTAAGTCTTAAAGACTTTGTTTGAATCTCCAGTTCC	4874
Qy	3660	TAGCATAGGCTGGCAGTGCAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGAAATATA	3719
Db	4875	TAGCATAGGCTGGCAGTGCAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGAAATATA	4934
Qy	3720	AACCTAGAAATATATCTTGTGTAATCAGACACCAAGTATGTCCTGTGTAAATGTGTGTA	3779
Db	4935	AACCTAGAAATATATCTTGTGTAATCAGACACCAAGTATGTCCTGTGTAAATGTGTGTA	4994
Qy	3780	C--GTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAAGATATATAGAACTATTTT	3833
Db	4995	CGTGTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAAGATATAGAACTATTTT	5055
Qy	3838	GGGGTATGGGTGCAATAATGGGAATGTTCTTTTAAAGAAATCTCCAAACGACTTCTG	3897
Db	5055	GGGGTATGGGTGCAATAATGGGAATGTTCTTTTAAAGAAATCTCCAAACGACTTCTG	5117
Qy	3898	GAAAGTATTTTCTAAGAACTTTGCTGGCAGGCTGAAGGCAACCCCTGTGTGCAAGGCC	3957
Db	5115	GAAAGTATTTTCTAAGAACTTTGCTGGCAGGCTGAAGGCAACCCCTGTGTGCAAGGCC	5177
Qy	3958	CACCCAGCTCAGCTGGGCACTCTGTCTTCCCAATGAAGGCTGTGCTCCCACTAATAT	4017
Db	5175	CACCCAGCTCAGCTGGGCACTCTGTCTTCCCAATGAAGGCTGTGCTCCCACTAATAT	5237
Qy	4018	ATTAATCTCTCTGGAGCTCAGGCAATGAGCAGCAAGGCAACCCATCCAGGCAACCTCTAG	4077
Db	5235	ATTAATCTCTCTGGAGCTCAGGCAATGAGCAGCAAGGCAACCCATCCAGGCAACCTCTAG	5297

[illegible]

Query Match	Best Local Similarity	Score	DB	Length	5300;
Matches 4082;	Conservative	0;	Mismatches	1;	Indels 2; Gaps 1;
1	GCTCCACGAGAGTCTCCCACTCTTAAGCTTTCGATCATCAGATGTTACGACGACGAGCTC	60			
1216	GCTCCACGAGAGTCTCCCACTCTTAAGCTTTCGATCATCAGATGTTACGACGACGAGCTC	1275			

QY 61 CGTAGGGTGAAGGCTGTGTCTTACACCTTGTATGCTTTACACCTGAGCTCACTGC 120  
 DB CGTAGGGTGAAGGCTGTGTCTTACACCTTGTATGCTTTACACCTGAGCTCACTGC 1335  
 QY 121 AACCTGCGCTCCAGGTTCAAGCAATTCTGTCTCAGGCTCCGCGTAGCTGAGACT 180  
 DB 1336 AACCTGCGCTCCAGGTTCAAGCAATTCTGTCTCAGGCTCCGCGTAGCTGAGACT 1395  
 QY 181 ACAGGCGCACGCGCGCTAATTTTTGTATGTTAGTAGAGATGGGGTTTCAACATATTAG 240  
 DB 1396 ACAGGCGCACGCGCGCTAATTTTTGTATGTTAGTAGAGATGGGGTTTCAACATATTAG 1455  
 QY 241 CCGGCGTGTCTTGAATCTCTGACCTCAGGTATCCACCCACTCAGCTCTTAAAGTGC 300  
 DB 1456 CCGGCGTGTCTTGAATCTCTGACCTCAGGTATCCACCCACTCAGCTCTTAAAGTGC 1515  
 QY 301 TGGGATTTACAGGCANTGAGTCAACGCGCGCCGCGCAAGGGTCAGTGTTTAAATAGGAATPAC 360  
 DB 1516 TGGGATTTACAGGCANTGAGTCAACGCGCGCCGCGCAAGGGTCAGTGTTTAAATAGGAATPAC 1575  
 QY 361 TTGAATGTTTACTAAACCAACAGGGAACAGACAAAAGCTGTGATTAATTTCAAGGATTC 420  
 DB 1576 TTGAATGTTTACTAAACCAACAGGGAACAGACAAAAGCTGTGATTAATTTCAAGGATTC 1635  
 QY 421 TTGGGATGGGAATGTGTCCATGAGCTGCTGCTAGTCCAGACACTGTGCTCATCA 480  
 DB 1636 TTGGGATGGGAATGTGTCCATGAGCTGCTGCTAGTCCAGACACTGTGCTCATCA 1695  
 QY 481 CTTCCTTCCTCATCTCATTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTGTG 540  
 DB 1696 CTTCCTTCCTCATCTCATTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTGTG 1755  
 QY 541 GTAAGCTTCAATCTGTACTGAATTAAGATATACATTAACCTAGTTTCATTTGGAGCCA 600  
 DB 1756 GTAAGCTTCAATCTGTACTGAATTAAGATATACATTAACCTAGTTTCATTTGGAGCCA 1815  
 QY 601 TCTGTGTGTGTATTAAGGGAGAGAGGCAATCCCAAGACCTCTTGAAGCCCGGAG 660  
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 DB 1876 AGGTTTCCTCTCAGCTGGGGAGCCCTGCAAGACCCGCGGTCTGTGGTGTCTGAGCA 1935  
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 DB 1936 ACCTGCGAGCCCGTGCACCTGTGTGTGTATCACTCTTGAAGGACCTGTGCTTTCT 1995  
 QY 781 ATTTCTGTGTGACTGTTCAATTCATCTCAGGCAATTCATTTGAATTAATTTAGATCTTATA 840  
 DB 1996 ATTTCTGTGTGACTGTTCAATTCATCTCAGGCAATTCATTTGAATTAATTTAGATCTTATA 2055  
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 DB 2116 GTGACAGTTTCTCATGGAAGAGCTGTGCAAGAAATTAATTAAGCCAGCCAACTTAAACCA 2175  
 QY 961 GTGTGTAAGAAAGAAATPAAACCACTTTGAAGATTTGTGGCGAGCTTCTTAAACA 1020  
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 DB 2236 GGGCACTCTCCTAGGGCCCGCTGTGCTCATCTGTGCGCGAGGCCCCAAGCCGAGT 2295  
 QY 1081 CTTCGAAGCTCTCTCTCATCATGATCAAGCGCTGAGAGCTGCGCTTCCGCTTCCGCTG 1140  
 DB 2296 CTTCGAAGCTCTCTCTCATCATGATCAAGCGCTGAGAGCTGCGCTTCCGCTTCCGCTG 2355

QY 1141 AATGCTCTGTGTCATCTGAGCTGAGACTCTTGTGCTCCAGGCTCCAGAAAGAAATGG 1200  
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 QY 1861 AAGGAGCAGAGCTGAGCACTGAGCCACAGGGAGGTGAGAGGGGACAGAAAGCACAG 1920  
 DB 3076 AAGGAGCAGAGCTGAGCACTGAGCCACAGGGAGGTGAGAGGGGACAGAAAGCACAG 3135  
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 DB 3136 CAGAACTGGGTGTCTCATCACTGTCTCATGTATCACTGACATCTCCAGAACCGAGGCA 3195  
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 QY 2221 AGGGAGGAGAAAGAAAGAGAGGATAGTGTATGAGCAAGAAAGACAGATTCATTCAG 2280





PD 26-JUN-2003.  
 XX 05-NOV-2001; 2001US-00985637.  
 XX 05-NOV-2001; 2001US-00985637.  
 PR (POLA/) POLANSKY J.  
 XX Polansky J;  
 PI WPI, 2004-031252/03.  
 PT Treatment of glaucomatous patient comprises administering non-steroidal  
 PT anti-inflammatory drug to patient.  
 XX Disclosure; SEQ ID NO 1; 32pp; English.  
 CC The invention relates to a method of treating glaucomatous patient  
 CC comprising determining whether the patient has a mutation in the TIGR  
 CC promoter consisting of TIGRm1 and/or TIGRm11 and administering a non-  
 CC steroidal anti-inflammatory drug to the patient. The method is useful for  
 CC the treatment of a glaucomatous patient, i.e. patient having glaucoma,  
 CC e.g. inherited glaucoma, or primary open angle glaucoma. The method  
 CC allows the identification of individuals at risk for progressive  
 CC increases in intraocular pressure, which is a risk factor for glaucoma.  
 CC It also allows the identification of individuals among ocular  
 CC hypertensive/glaucoma suspect groups at increased risk of visual field  
 CC loss. The present sequence represents the human TIGR promoter DNA.  
 CC  
 SQ Sequence 5300 BP; 1482 A; 1152 C; 1235 G; 1431 T; 0 U; 0 Other;  
 Query Match 67.8%; Score 4069.4; DB 12; Length 5300;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;  
 QY 1 GCTCCACAGAAAGTCTCCCACTTAGAATTGTCATCAACATGTTACAGCCAGAGCTC 60  
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 DB 1396 ACAGGCGCACGCGCCGGCTAATTTTGTATTGTAGTAGAGATGGGGTTTCAACATATTAG 1455  
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DB 1756 GTAAAGCTCCACATCGTTACTGAATTAAGATATACATAAATTAAGTTCCATTTGGGGCCA 1815  
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Db 5056 GCGATGGCTCAAAATGGAATCTTTTAAAAAGAACTCAAGACGCTTCGG 5115
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Db 5116 AAGTTATTTTCTAAGATCTTCTGCGACGCTGAAGCAACCCCTGTGCACAGCCC 5175
Qy 3959 ACCGAGCTCAAGTGGGCACTCTGTCTTCCCAATGAAGGCTGCTCCCACTATATA 4018
Db 5176 ACCGAGCTCAAGTGGGCACTCTGTCTTCCCAATGAAGGCTGCTCCCACTATATA 5235
Qy 4019 TAAACCTCTGAGCTGAGGCAATGAGCCAGCAAGCCCATCTCAGGCACTCTCAGC 4078
Db 5236 TAAACCTCTGAGGCTGAGGCAATGAGCCAGCAAGCCCATCTCAGGCACTCTCAGC 5295
Qy 4079 ACAGC 4083
Db 5296 ACAGC 5300

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## RESULT 7

ADQ15241  
ID ADQ15241 standard; DNA; 5300 BP.

AC ADQ15241;

DT 23-SEP-2004 (first entry)

DE Human trabecular meshwork glucocorticoid response, TIGR, 5' region.

DM Human; de; trabecular meshwork glucocorticoid response; TIGR, 5' region;

KM glaucoma; SNP; single nucleotide polymorphism;

KM non-steroidal anti-inflammatory drug; NSAID; intraocular pressure;

KM inherited glaucoma; open angle glaucoma; primary open angle glaucoma;

KM ocular inflammation.

OS Homo sapiens.

XX Key Location/Qualifiers

FT variation replace(4337,G)

FT /tag= a /standard\_name= "Single nucleotide polymorphism"

FT variation replace(5113,C)

FT /tag= b /standard\_name= "Single nucleotide polymorphism"

FT US2004132795-A1.

PN 08-JUL-2004.

PD 22-DEC-2003; 2003US-00741339.

PF 05-NOV-2001; 2001US-00985637.

PR (POLA/) POLANSKY J.

XX Polansky J;

PI WPI; 2004-542638/52.

DR Treatment of glaucomatous patient involves determining whether patient

PT has a mutation in trabecular meshwork glucocorticoid response promoter,

PT followed by administration of non-steroidal anti-inflammatory drug.

XX Disclosure; SEQ ID NO 1; 31pp; English.

PS The invention relates to a method of providing treatment to a

CC glaucomatous patient involves (a) determining whether the patient has a

CC mutation in the trabecular meshwork glucocorticoid response (TIGR)

CC promoter selected from TIGRnt1, TIGRnt11, or both TIGRnt1 and TIGRnt11

CC and (b) administering a non-steroidal anti-inflammatory drug (NSAID) to

CC the patient. Also included are a method of preventing increases in

CC intraocular pressure in a patient predisposed to developing glaucoma, a

CC method for decreasing the mean diurnal intra-ocular pressure in a  
CC patient, a method of providing treatment to a patient known to possess at  
CC least one mutation in the TIGR gene selected from TIGRnt1 and TIGRnt11,  
CC a method of selecting a patient for a clinical trial, a method of  
CC improving the results of a drug study involving a treatment for elevated  
CC intraocular pressure, a method of determining whether a patient is at  
CC risk for developing elevated intraocular pressure, and a method of  
CC testing the efficacy of a therapeutic agent at counteracting glaucoma  
CC pathogenic mechanisms. The methods are used for preventing increases in  
CC intraocular pressure in a patient (i.e. a patient having asymptomatic  
CC glaucoma) predisposed to developing glaucoma (such as an inherited  
CC glaucoma, an open angle glaucoma (e.g. primary open angle glaucoma), for  
CC decreasing the mean diurnal intra-ocular pressure in a patient and the  
CC treatment of ocular inflammation. The method allows the identification of  
CC individuals at risk for progressive increase in intraocular pressure and  
CC thus allows the identification of individuals among ocular  
CC hypertensive/glaucoma suspect groups at increased risk of visual field  
CC loss. The present sequence is the 5' region of the human TIGR gene.

SO Sequence 5300 BP; 1482 A; 1152 C; 1235 G; 1431 T; 0 U; 0 Other;

Query Match 67.8%; Score 4069.4; DB 12; Length 5300;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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Qy 1 GCTCCACAGGAAGTCTCCCACTAGACTTTCGATCAGATGTATACAGCCAGAACTC 60
Db 1216 GCTCCACAGGAAGTCTCCCACTAGACTTTCGATCAGATGTATACAGCCAGAACTC 1275
Qy 61 CGTAGAGGTGAGGCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTACTGC 120
Db 1276 CGTAGAGGTGAGGCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTACTGC 1335
Qy 121 AACCTGCTCCCAAGGTTAAGCAATTCCTGCTCAGCTCCGCGTAGCTGGAGACT 180
Db 1336 AACCTGCTCCCAAGGTTAAGCAATTCCTGCTCAGCTCCGCGTAGCTGGAGACT 1395
Qy 181 ACAGGCGCAGCCCGGCTAATTTTGTATTTGTATAGATAGGGGTTTACCATATTAG 240
Db 1396 ACAGGCGCAGCCCGGCTAATTTTGTATTTGTATAGATAGGGGTTTACCATATTAG 1455
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 Db 3556 GCTATATTTGTGGGGGAGAAATCAGTTCAAGGAGAGTGGGAGACCTGATTTCTAATAC 3615  
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 Db 3616 TATATTTTCTCTTAAAGAGTGAATTTCTGAGCAAGTCAAGATGTAATCTAGGCT 3675  
 QY 2461 GTAAGATTAAGTATTTCTCTTAAAGAGTGAATTTCTGAGCAAGTCAAGATGTAATCTAGGCT 2520  
 Db 3676 GTAAGATTAAGTATTTCTCTTAAAGAGTGAATTTCTGAGCAAGTCAAGATGTAATCTAGGCT 3735  
 QY 2521 AAGGCAATCCGTTCTTTTAAAGAGAGAAACATTCCTAAGATTAAGCAACAGAT 2580  
 Db 3736 AAGGCAATCCGTTCTTTTAAAGAGAGAAACATTCCTAAGATTAAGCAACAGAT 3795  
 QY 2581 TCAAGCCTAAGTCTTGTGACTGACTATATGATGTTTTTGAATAATCATTCAGCATGTT 2640  
 Db 3796 TCAAGCCTAAGTCTTGTGACTGACTATATGATGTTTTTGAATAATCATTCAGCATGTT 3855  
 QY 2641 TACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAACCCAT 2700  
 Db 3856 TACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAACCCAT 3915  
 QY 2701 TTGTAAATGTCTCAAGTTCAAGCTTAACTGAGAACCAATCAATTAATTAATGAATCTTT 2760  
 Db 3916 TTGTAAATGTCTCAAGTTCAAGCTTAACTGAGAACCAATCAATTAATTAATGAATCTTT 3975  
 QY 2761 AAGAGCAATCTGTGTTCTCACTGAGAGTGAAGTGTGCAAGGCAAGTTTGAATAATTT 2820  
 Db 3976 AAGAGCAATCTGTGTTCTCACTGAGAGTGAAGTGTGCAAGGCAAGTTTGAATAATTT 4035  
 QY 2821 ACTTCAGAAAGTATGACCTGTGTGTATTAACAATAAGTGTCAAAAGCAATC 2880  
 Db 4036 ACTTCAGAAAGTATGACCTGTGTGTATTAACAATAAGTGTCAAAAGCAATC 4095  
 QY 2881 ATTATTTCAAGTGGCTTAAAGTAACTTCTGACAGTTTGTATTAATTTATGAGCTATGCC 2940



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Db      4096 ATTATTCAGAGTGGCTTAAAGTTACTTCGACAGTTTTGTATATTATGCTATATGCC 4155
Qy      2941 ATTGCTTTTGGTTTCTCTTGGGTTTATATGTAAGCAGGATTAATTAACCTAC 3000
Db      4156 ATTGCTTTTGGTTTCTCTTGGGTTTATATGTAAGCAGGATTAATTAACCTAC 4215
Qy      3001 AGTCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTTTTACCACTT 3060
Db      4216 AGTCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTACATTTTGTTTTACCACTT 4275
Qy      3061 CTAACTAAATTTTAACTTTTATTCATTGCGAATAGACCATAAAGCTGAATATA 3120
Db      4276 CTAACTAAATTTTAACTTTTATTCATTGCGAATAGACCATAAAGCTGAATATA 4335
Qy      3121 ACAGTACCTGTGATTGTGCAATTACCAATAGAAATCAGACATTTTATGATATATCA 3180
Db      4336 ACAGTACCTGTGATTGTGCAATTACCAATAGAAATCAGACATTTTATGATATATCA 4395
Qy      3181 GTTGTGAGAGTACCTGTGAAGTGAATTTATCTCAAAACTATCTTGAATTTAGACC 3240
Db      4396 GTTGTGAGAGTACCTGTGAAGTGAATTTATCTCAAAACTATCTTGAATTTAGACC 4455
Qy      3241 TCTGCTGAGATCTGTTTAACTATTAATAAATGTTTAAATTTGATATTTTGA 3300
Db      4456 TCTGCTGAGATCTGTTTAACTATTAATAAATGTTTAAATTTGATATTTTGA 4515
Qy      3301 TAAATATTTTCAATATCATTTGTTCTCTTGTATCTATATTTATTAATTTGAAAAA 3360
Db      4516 TAAATATTTTCAATATCATTTGTTCTCTTGTATCTATATTTATTTGAAAAA 4575
Qy      3361 TCTTCTGAGAGAGTCCCGAGATTTTCAACAATGAGTTCTTGGCATGACACACAG 3420
Db      4576 TCTTCTGAGAGAGTCCCGAGATTTTCAACAATGAGTTCTTGGCATGACACACAG 4635
Qy      3421 AGTAAAGAACTGATTTAGAGGCTTAACATTGACATTTGCTGCTGAGATGCAAGCTGAATT 3480
Db      4636 AGTAAAGAACTGATTTAGAGGCTTAACATTGACATTTGCTGCTGAGATGCAAGCTGAATT 4695
Qy      3481 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAAGGGGGGAAATCTGC 3540
Db      4696 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTAAGGGGGGAAATCTGC 4755
Qy      3541 CGCTTCTATAGAAATGCTCTCCCTGAGAGCTGTAGAGTGTCTGTTGTCTGAGCTG 3600
Db      4756 CGCTTCTATAGAAATGCTCTCCCTGAGAGCTGTAGAGTGTCTGTTGTCTGAGCTG 4815
Qy      3601 GCTGTTATTTTCTCTGCTGCTGCTACGCTTTAAAGAACTTTTGGATCTCCAGTTCT 3660
Db      4816 GCTGTTATTTTCTCTGCTGCTGCTACGCTTTAAAGAACTTTTGGATCTCCAGTTCT 4875
Qy      3661 AGCATAGTCCCTGGGACAGTGAAGTTCTCAATGAGTTTGCAGAGTAATGAAATATTA 3720
Db      4876 AGCATAGTCCCTGGGACAGTGAAGTTCTCAATGAGTTTGCAGAGTAATGAAATATTA 4935
Qy      3721 ACTAGAAATATATCTTGTGTAATCAGACACAGTACTCTGTGTATAGTGTGTAC 3780
Db      4936 ACTAGAAATATATCTTGTGTAATCAGACACAGTACTCTGTGTATAGTGTGTAC 4995
Qy      3781 --GTGTGTGTGTGTGTGTGTGTGTAAAACAGGTGAGATATAGAACTATATTG 3838
Db      4996 GTGTGTGTGTGTGTGTGTGTGTGTAAAACAGGTGAGATATAGAACTATATTG 5055
Qy      3839 GGGTATAGGATGAATAATTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGC 3898
Db      5056 GGGTATAGGATGAATAATTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGC 5115
Qy      3899 AAGGTATTTTCTAAGAACTTGTGCTGAGCGTGAAGCAACCCCTGTGACAGCCCC 3958
Db      5116 AAGGTATTTTCTAAGAACTTGTGCTGAGCGTGAAGCAACCCCTGTGACAGCCCC 5175
Qy      3959 ACCAGCCTCAGTGCGCACTCTGTCTTCCCATGAAGAGGTGCTCCCATGATATTA 4018
Db      5176 ACCAGCCTCAGTGCGCACTCTGTCTTCCCATGAAGAGGTGCTCCCATGATATTA 5235

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Qy      4019 TAAACCTCTCTGAGCTCAGGCATGACAGCAAGGCCACCATTCAGGCACTCTCAGC 4078
Db      5236 TAAACCTCTCTGAGGCTCGGGCATGACCAAGCAAGCCATTCAGGCACTCTCAGC 5295
Qy      4079 ACAGC 4083
Db      5296 ACAGC 5300

RESULT 8
AAVS1361
ID  AAVS1361 standard; DNA; 5299 BP.
XX
XX
AC  AAVS1361;
XX
XX  27-OCT-1998 (first entry)
DT
DE  Human TIGR promoter region DNA.
XX
XX  TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW  diagnosis; glaucoma; polymorphism; steroid sensitivity; ss.
XX
OS  Homo sapiens.
XX
PN  M09832850-A1.
XX
PD  30-JUL-1998.
XX
PF  09-JAN-1998; 98WO-US000468.
XX
PR  28-JAN-1997; 97US-00791154.
PR  26-SEP-1997; 97US-00938669.
XX
PA  (RBCG ) UNIV CALIFORNIA.
XX
PI  Nguyen TD, Polansky JR, Chen P, Chen H;
XX
DR  WPI, 1998-427946/36.
XX
PT  Use of TIGR nucleic acid sequences - used for, e.g. developing products
PT  for diagnosis, prognosis and treatment of glaucoma.
XX
PS  Claim 34; Fig 1; 105bp; English.
CC  This sequence is a trabecular meshwork induced glucocorticoid response
CC  protein (TIGR) promoter region which is used in a method for diagnosing
CC  glaucoma in a patient. The method involves the detection of polymorphisms
CC  whose presence is predictive of a mutation affecting TIGR response in the
CC  patient and can be diagnostic of glaucoma or steroid sensitivity. Base
CC  substitutions and base additions upstream of and within TIGR exons can
CC  also be used to diagnose glaucoma
XX
SQ  Sequence 5299 BP; 1482 A; 1151 C; 1235 G; 1431 T; 0 U; 0 Other;

Query Match      67.8%; Score 4068.4; DB 2; Length 5299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy      1 GCTCCAGAGAAAGTCTCCCACTCTAGACTTCTGCATCAAGATTTACAGCCAGAAAGCTC 60
Db      1216 GCTCCAGAGAAAGTCTCCCACTCTAGACTTCTGCATCAAGATTTACAGCCAGAAAGCTC 1275
Qy      61 CGTGAAGGATGAGGCTGTGTCTTACACTCACTGATAGTCTCTACACCTGAGCTCACTGC 120
Db      1276 CGTGAAGGATGAGGCTGTGTCTTACACTCACTGATAGTCTCTACACCTGAGCTCACTGC 1335
Qy      121 AACCTCTGCTCCAGGTTCAAGCAATCTCTGTCTCAGCTCCCGGTAGCTGGAAT 180
Db      1336 AACCTCTGCTCCAGGTTCAAGCAATCTCTGTCTCAGCTCCCGGTAGCTGGAAT 1395
Qy      181 ACAGGCGCAGCGCCGCTAATTTTGTATTTGTAAGATGAGATGGGTTTACCATATTAG 240

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Db 1396 ACAGGGCACGCCCCGCTAATTTTGTATGTAAGATGGGGTTTCACCATATATAG 1455  
QY 241 CCCGGCTGCTTGAATCTCCTGACCTCAGGGTATCCACCCACCTCAGCCTCTTAAGTGC 300  
Db 1456 CCGGGCTGGCTTGAATCTCCTGACCTCAGGGTATCCACCCACCTCAGCCTCTTAAGTGC 1515  
QY 301 TGGGATTAACAGGACATGATCAGCGCGCCGGCCAGGGGTGATGTTTAATPAAGAAATAC 360  
Db 1516 TGGGATTAACAGGACATGATCAGCGCGCCGGCCAGGGGTGATGTTTAATPAAGAAATAC 1575  
QY 361 TTGAATGTTTACTTAACCAACAGGAAACAGACAAAGCTGTGATTAATTCAGGGATTC 420  
Db 1576 TTGAATGTTTACTTAACCAACAGGAAACAGACAAAGCTGTGATTAATTCAGGGATTC 1635  
QY 421 TTGGGATGGGGAAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGCTCTCATCA 480  
Db 1636 TTGGGATGGGGAAATGGTGCCATGAGCTGCTGCTAGTCCAGACCACTGCTCTCATCA 1695  
QY 481 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTATTCACATGCTTTTGTG 540  
Db 1696 CTTTCTTCCCTCATCTCATTTTCAAGGCTAAGTTACATTTTATTCACATGCTTTTGTG 1755  
QY 541 GTAAGCTCCACATCTGTTACTGAAATPAAGATATACATAAATAGTTCCATTTGGGGCCA 600  
Db 1756 GTAAGCTCCACATCTGTTACTGAAATPAAGATATACATAAATAGTTCCATTTGGGGCCA 1815  
QY 601 TCTGTGTGTGTATAGGGGAGGAGGACATCCCAAGACCTCTTGAAGCCCCCGGACAG 660  
Db 1816 TCTGTGTGTGTATAGGGGAGGAGGACATCCCAAGACCTCTTGAAGCCCCCGGACAG 1875  
QY 661 AAGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGCTGAGCA 720  
Db 1876 AAGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCTGGGTGCTGAGCA 1935  
QY 721 ACTGCGCAACCCGCTGACCTGCTGTTTGTGTTATCACTCTCTAGGACCTGTTGCTTCT 780  
Db 1936 ACTGCGCAACCCGCTGACCTGCTGTTTGTGTTATCACTCTCTAGGACCTGTTGCTTCT 1995  
QY 781 ATTTCTGTGTGACTGCTTCAATTCATTCAGGCAATTCATGCAATTAATGAGTAACTTAA 840  
Db 1996 ATTTCTGTGTGACTGCTTCAATTCATTCAGGCAATTCATGCAATTAATGAGTAACTTAA 2055  
QY 841 TCTGCCAGACACGAGACAAATATGTTGAGCAAGACGTCATGCTTACCTTCTGTTGAG 900  
Db 2056 TCTGCCAGACACGAGACAAATATGTTGAGCAAGACGTCATGCTTACCTTCTGTTGAG 2115  
QY 901 GTGACAGTTTCTCATGGAAGAAGTGTGAGAAATTAATAGCAGCCCACTTAAACCA 960  
Db 2116 GTGACAGTTTCTCATGGAAGAAGTGTGAGAAATTAATAGCAGCCCACTTAAACCA 2175  
QY 961 GTGCTGAAGAAGAAATPAACACATCTTGAAGATTTGTGGAGCATGCCCTTAACA 1020  
Db 2176 GTGCTGAAGAAGAAATPAACACATCTTGAAGATTTGTGGAGCATGCCCTTAACA 2235  
QY 1021 GGGCACTTCCCTAGCGCCCCCTGCTGCTCATCTGTCGCCGAGGCCCAAGCCCGAGT 1080  
Db 2236 GGGCACTTCCCTAGCGCCCCCTGCTGCTCATCTGTCGCCGAGGCCCAAGCCCGAGT 2295  
QY 1081 CTTTCCAGGCTCTCTCTCATCATGATCAAGCGCTGTGAGCTGGCTGCTGCTTCCCGTG 1140  
Db 2296 CTTTCCAGGCTCTCTCTCATCATGATCAAGCGCTGTGAGCTGGCTGCTGCTTCCCGTG 2355  
QY 1141 AATGCTCTGTGATCTGTAGCTGAGACTCTGTTGGCTCAGGCTCCAGAAAGAAATAG 1200  
Db 2356 AATGCTCTGTGATCTGTAGCTGAGACTCTGTTGGCTCAGGCTCCAGAAAGAAATAG 2415  
QY 1201 AGAGGAAAATAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTGTTCTCAGAGGAAAGG 1260  
Db 2416 AGAGGAAAATAGTCTTAACGAGAAATCTGAGAGGGAACAGTGTGTTCTCAGAGGAAAGG 2475  
QY 1261 GCTTCAACGTCCAGAGAAATTCAGAGAGGTGGGACTGTGAGAGAGTGGGGAAGCTTGGGGC 1320  
Db 2476 GCTTCAACGTCCAGAGAAATTCAGAGAGGTGGGACTGTGAGAGAGTGGGGAAGCTTGGGGC 2535

QY 1321 TGAGCGGGTGTGAAGAGGAGAGTGAAGAGGGGCAAGGCTGAAGCTCCAGATGTTCC 1380  
Db 2536 TGAGCGGGTGTGAAGAGGAGAGTGAAGAGGGGCAAGGCTGAAGCTCCAGATGTTCC 2595  
QY 1381 AGTGTGTTCAAGGGGCTGGAGTGTTCGTTGCTTCTCTGTGAGCTCTTTTATCTTTCT 1440  
Db 2596 AGTGTGTTCAAGGGGCTGGAGTGTTCGTTGCTTCTCTGTGAGCTCTTTTATCTTTCT 2655  
QY 1441 CTGCTTGAAGAGAGAAAGTCTATTTTATGAAGGATGCAAGTTTCATPAAGTCACTGTT 1500  
Db 2656 CTGCTTGAAGAGAGAAAGTCTATTTTATGAAGGATGCAAGTTTCATPAAGTCACTGTT 2715  
QY 1501 AAAATTCAGGGGCTGATGGGTTTCTTCCAGAGGCTTATTTAATGGAAATATAG 1560  
Db 2716 AAAATTCAGGGGCTGATGGGTTTCTTCCAGAGGCTTATTTAATGGAAATATAG 2775  
QY 1561 GAAGCAGCTCATTTCTTAGGCCGTTAATTCAGAGAAAGTGAATGAGTCTTTCTTT 1620  
Db 2776 GAAGCAGCTCATTTCTTAGGCCGTTAATTCAGAGAAAGTGAATGAGTCTTTCTTT 2835  
QY 1621 CATGCTTCTGGGCAACTACTAGCCCTGTGTGAATCTTGGCTTATGCAAGCGTCTGA 1680  
Db 2836 CATGCTTCTGGGCAACTACTAGCCCTGTGTGAATCTTGGCTTATGCAAGCGTCTGA 2895  
QY 1681 AACCTTGAATCAGAGAGACTGGGTTTCTTCTGTTCTGCAATGGTTGGCTGTGCGAC 1740  
Db 2896 AACCTTGAATCAGAGAGACTGGGTTTCTTCTGTTCTGCAATGGTTGGCTGTGCGAC 2955  
QY 1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCTTAAAGACCTTTGCA 1800  
Db 2956 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGCTTAAAGACCTTTGCA 3015  
QY 1801 GCTCTGTGTGTTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAAGGGG 1860  
Db 3016 GCTCTGTGTGTTGTGAACATTTCCCTGTGATTTCTGTGAGGGGGAGTGTGAAGGGG 3075  
QY 1861 AAGGAGGAGAGCTGAGAGAGCTGAGCCACAGGGAGGTGTGAGGGGAGACAGAAAGCAG 1920  
Db 3076 AAGGAGGAGAGCTGAGAGAGCTGAGCCACAGGGAGGTGTGAGGGGAGACAGAAAGCAG 3135  
QY 1921 CAGAACTGGGTGCTCCATCAGTCTCTCACTGATCAAGTCAAGCTCCAGAGCCGAGGCA 1980  
Db 3136 CAGAACTGGGTGCTCCATCAGTCTCTCACTGATCAAGTCAAGCTCCAGAGCCGAGGCA 3195  
QY 1981 CAATCTTCAAGAAAGTCTCATGAACCAACAGCCAACTTTTCTTCCCTAAGCATAGAC 2040  
Db 3196 CAATCTTCAAGAAAGTCTCATGAACCAACAGCCAACTTTTCTTCCCTAAGCATAGAC 3255  
QY 2041 AATGGCATTTGCGCAATTAACCAAAAGAAATGCAAGACCTTAATGCTGTTTGGCTG 2100  
Db 3256 AATGGCATTTGCGCAATTAACCAAAAGAAATGCAAGACCTTAATGCTGTTTGGCTG 3315  
QY 2101 GCATTCAAAATCTGGGCAAGAGCAAGTGAAGAAATGCCAGAGATTTGTTAACTTTTCAACC 2160  
Db 3316 GCATTCAAAATCTGGGCAAGAGCAAGTGAAGAAATGCCAGAGATTTGTTAACTTTTCAACC 3375  
QY 2161 TGAACAGACCCCAAGCTCAGAGTGAAGTGTCTGACAGCAAGGAGTGAAGCTGAGCGC 2220  
Db 3376 TGAACAGACCCCAAGCTCAGAGTGAAGTGTCTGACAGCAAGGAGTGAAGCTGAGCGC 3435  
QY 2221 AGGGAGGAGAAAGAAAGAGAGGATGTGTATAGCAAGAAAGACAGATTCATTCAAG 2280  
Db 3436 AGGGAGGAGAAAGAAAGAGAGGATGTGTATAGCAAGAAAGACAGATTCATTCAAG 3495  
QY 2281 GGCAGTGGAAATTTGACACAGGGAATTAATAGTCCAGTATCTGTGGTTCTAGAGAGCAGG 2340  
Db 3496 GGCAGTGGGAATTTGACACAGGGAATTAATAGTCCAGTATCTGTGGTTCTAGAGAGCAGG 3555  
QY 2341 GCTATATTTGTGGGGGAAAAAATCATGAGGAAAGTGGGAGACTGATTTCTAATATAC 2400  
Db 3556 GCTATATTTGTGGGGGAAAAAATCATGAGGAAAGTGGGAGACTGATTTCTAATATAC 3615

QY	2401	TATATTTTCTCTTACAAAGCTGAGTAATTCTGAGCAAGTCAAGGTAGTAACAGGCT	2460
Db	3616	TATATTTTCTCTTAAACAAGCTGAGTAATTCTGAGCAAGTCAAGGTAGTAACAGGCT	3675
QY	2461	GTAAGATCTACTAGTTTCTCCCTATATTAGAACTCTTTTCTCTGAGAGTTAGAGCACA	2520
Db	3676	GTAAGATCTACTAGTTTCTCCCTATATTAGAACTCTTTTCTCTGAGAGTTAGAGCACA	3735
QY	2521	AGGGCAATCCGGTTTCTTTTAAACAGAAAGAAAACATTCCTAAGATAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCGGTTTCTTTTAAACAGAAAGAAAACATTCCTAAGATAAGCCAAACAGAT	3795
QY	2581	TCAAGCCTAAGGCTCTTGCTGCACTATATGATGGTTTTTGA AAAATCATTTACGGAGTGT	2640
Db	3786	TCAAGCCTAAGGCTCTTGCTGCACTATATGATGGTTTTTGA AAAATCATTTACGGAGTGT	3855
QY	2641	TACTATCTGATTCAGAAAATGAGACTAGAACCCCTTGCTGAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAAATGAGACTAGAACCCCTTGCTGAGCTGTAAACAAACCCAT	3915
QY	2701	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAGAACCAATCAATTAAGAAATAGATCTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAAGCTTAACTGCAGAACCAATCAATTAAGAAATAGATCTTT	3975
QY	2761	AGAGCAAACTGTGTCTTCCCACTCTGAGAGTGAGTCTCCAGGGCAGTTTGAAATATTT	2820
Db	3976	AGAGCAAACTGTGTCTTCCCACTCTGAGAGTGAGTCTCCAGGGCAGTTTGAAATATTT	4035
QY	2821	ACTTCAACAAGTATGACACTGTGTGTGGATTTAACAATTAAGTTGTCTCAAGGCAATC	2880
Db	4036	ACTTCAACAAGTATGACACTGTGTGTGGATTTAACAATTAAGTTGTCTCAAGGCAATC	4095
QY	2881	ATTATTTTCAAGTGCTTAAAGTTACTCTGACAGTTTGTGATATTTATTTGGCTATTGGC	2940
Db	4096	ATTATTTTCAAGTGCTTAAAGTTACTCTGACAGTTTGTGATATTTATTTGGCTATTGGC	4155
QY	2941	ATTTGCTTTTGTTTTTCTCTTGGGTTATTTATGTAAGACAGGATTTATTAACCTAC	3000
Db	4156	ATTTGCTTTTGTTTTTCTCTTGGGTTATTTATGTAAGACAGGATTTATTAACCTAC	4215
QY	3001	AGTCAGAAAGCCTGAGATTGTAATGAGAAAAATTACAATTTTGTTTTACACCTT	3060
Db	4216	AGTCAGAAAGCCTGAGATTGTAATGAGAAAAATTACAATTTTGTTTTACACCTT	4275
QY	3061	CTAATCAATTTAACAATTTATTTCCATTGCGAATAGAGCCATTAACCTCAAGTGGTATA	3120
Db	4276	CTAATCAATTTAACAATTTATTTCCATTGCGAATAGAGCCATTAACCTCAAGTGGTATA	4335
QY	3121	ACAGTACCTGTGATTTTGTCAATTAACCATAGAAATCAAGACATTTTATCTATTTACA	3180
Db	4336	ACAGTACCTGTGATTTTGTCAATTAACCATAGAAATCAAGACATTTTATCTATTTACA	4395
QY	3181	GTTGTGACAGATCGTTGAAGTGAATATTTATCTCAAAACTACTTGAATTTAGAC	3240
Db	4396	GTTGTGACAGATCGTTGAAGTGAATATTTATCTCAAAACTACTTGAATTTAGAC	4455
QY	3241	TCCGTGCGATCTGTTTTTAAACATATTAATAAACAATGTTAAATTTGATATTTGCA	3300
Db	4456	TCCGTGCGATCTGTTTTTAAACATATTAATAAACAATGTTAAATTTGATATTTGCA	4515
QY	3301	TATCATATTTCAATTAATCAATTTGTTCTTTGTAATCTATATTTTATATTTGAAAACA	3360
Db	4516	TATCATATTTCAATTAATCAATTTGTTCTTTGTAATCTATATTTTATATTTGAAAACA	4575
QY	3361	TCTTTCTGAGAAAGTCCCAAGATTTTCAACAATAGATGTTCTTGGCATGACACACAG	3420
Db	4576	TCTTTCTGAGAAAGTCCCAAGATTTTCAACAATAGATGTTCTTGGCATGACACACAG	4635
QY	3421	AGTGAAGATGATTTTGAAGGCTTAACATTTGACATTTGGTGCCTGAGATGCAAGCTAATTT	3480
Db	4636	AGTGAAGATGATTTTGAAGGCTTAACATTTGACATTTGGTGCCTGAGATGCAAGCTAATTT	4695
QY	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTTAAAGCTAAGGGTGAAGGGGAAATCTGC	3540

[illegible]

XX (REGC ) UNIV CALIFORNIA.  
XX Nguyen TD, Polansky JR, Chen P, Chen H;  
XX WPI; 1998-427946/36.  
XX  
XX Use of TIGR nucleic acid sequences - used for, e.g. developing products  
XX for diagnosis, prognosis and treatment of glaucoma.  
XX  
XX Disclosure; Fig 2; 105dp; English.  
XX  
XX This sequence is a trabecular meshwork induced glucocorticoid response  
XX protein (TIGR) promoter mutant, TIGRm4, which is used in a method for  
XX diagnosing glaucoma in a patient. The method involves the detection of  
XX polymorphisms whose presence is predictive of a mutation affecting TIGR  
XX response in the patient and can be diagnostic of glaucoma or steroid  
XX sensitivity. Base substitutions and base additions upstream of and within  
XX TIGR exons can also be used to diagnose glaucoma  
XX  
XX Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;  
SQ  
Query Match 67.8%; Score 4067.8; DB 2; Length 5300;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;  
QY 1 GCTCCAGAGAGTCCCACTCTAGACTTTCAGATCAGATGTTACAGCCAGAAAGCTC 60  
DB 1216 GCTCCAGAGAGTCCCACTCTAGACTTTCAGATCAGATGTTACAGCCAGAAAGCTC 1275  
QY 61 CGTGAAGGTGAGGGTCTGTGTCTTACACCTACCTGATGCTCTACAGCTGACTGCG 120  
DB 1276 CGTGAAGGTGAGGGTCTGTGTCTTACACCTACCTGATGCTCTACAGCTGACTGCG 1335  
QY 121 AACCTTGCTCTCCAGATTAACCAATTCCTGTCTCAGCTCCGCGTGAAGTGGAGCT 180  
DB 1336 AACCTTGCTCTCCAGATTAACCAATTCCTGTCTCAGCTCCGCGTGAAGTGGAGCT 1395  
QY 181 ACAGGGCAGCGCCGGCTAATTTTGTATGATGATGAGATGGGGTTTCAACATATTAG 240  
DB 1396 ACAGGGCAGCGCCGGCTAATTTTGTATGATGATGAGATGGGGTTTCAACATATTAG 1455  
QY 241 CCCGGCTGTGTTGAACTCCTGACCTCAGGTATCCACCCACCTCAGCTCTTAAAGTGC 300  
DB 1456 CCCGGCTGTGTTGAACTCCTGACCTCAGGTATCCACCCACCTCAGCTCTTAAAGTGC 1515  
QY 301 TGGGATTAACGAGATGATGATCCGCGCCCGGAGGATGATGTTTAAATAGGAATTAAC 360  
DB 1516 TGGGATTAACGAGATGATGATCCGCGCCCGGAGGATGATGTTTAAATAGGAATTAAC 1575  
QY 361 TGAATGTTTCTAACAACAAGGGAACAAGCAAAAGCTGTGATTAATTTTCAAGGATTC 420  
DB 1576 TGAATGTTTCTAACAACAAGGGAACAAGCAAAAGCTGTGATTAATTTTCAAGGATTC 1635  
QY 421 TTGGGATGAGGAAATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 1636 TTGGGATGAGGAAATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1695  
QY 481 CTTTCTTCCCTCACTCTCAATTTTCAAGGCTAAGTTTACATTTTATTCACCATGCTTTTGG 540  
DB 1696 CTTTCTTCCCTCACTCTCAATTTTCAAGGCTAAGTTTACATTTTATTCACCATGCTTTTGG 1755  
QY 541 GTTAAGCTTCACATGTTTCTAATAAATAAGATTAACATAAATAGTTTCAATTTTGGGCA 600  
DB 1756 GTTAAGCTTCACATGTTTCTAATAAATAAGATTAACATAAATAGTTTCAATTTTGGGCA 1815  
QY 601 TCTGTGTGTGTATATAGGAGAGAGGCAATACCCAGAGACTCTTGAAGCCCGGCGAG 660  
DB 1816 TCTGTGTGTGTATATAGGAGAGAGGCAATACCCAGAGACTCTTGAAGCCCGGCGAG 1875  
QY 661 AAGTTTCTCTCTCAAGTGGGGAGCCCTGCAAGCAACCCGGGCTCTGGGTGTCTGAGCA 720  
DB 1876 AAGTTTCTCTCTCAAGTGGGGAGCCCTGCAAGCAACCCGGGCTCTGGGTGTCTGAGCA 1935

QY 721 ACCGCAAGCCCGTGGCACTGATGTTTGTATGACTGCTTAGAGGACCTGTGCTTCT 780  
DB 1936 ACCGCAAGCCCGTGGCACTGATGTTTGTATGACTGCTTAGAGGACCTGTGCTTCT 1995  
QY 781 ATTCTGTGTGACTCTGTTCAATTCATCCAGGATTCATGACATTAATTAAGTACTTATA 840  
DB 1996 ATTCTGTGTGACTCTGTTCAATTCATCCAGGATTCATGACATTAATTAAGTACTTATA 2055  
QY 841 TCTGCCAGACACCAAGACAAATATGTTGACAAAGCATGCTGCTTACCTTGTGGAG 900  
DB 2056 TCTGCCAGACACCAAGACAAATATGTTGACAAAGCATGCTGCTTACCTTGTGGAG 2115  
QY 901 GTGACAGTTTTCATATGAGAGAGTGTGAGAGAAATTAATTAAGCACCACCTTAACCCA 960  
DB 2116 GTGACAGTTTTCATATGAGAGAGTGTGAGAGAAATTAATTAAGCACCACCTTAACCCA 2175  
QY 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGCAGCATTCCTTAACA 1020  
DB 2176 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGCAGCATTCCTTAACA 2235  
QY 1021 GGCCACTCTCTAGCGCCCTGTGCTGCTCATTCGTGCCGAGGCCCAAGCCGAGT 1080  
DB 2236 GGCCACTCTCTAGCGCCCTGTGCTGCTCATTCGTGCCGAGGCCCAAGCCGAGT 2295  
QY 1081 CTTCCAGGCTCTCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1140  
DB 2296 CTTCCAGGCTCTCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 2355  
QY 1141 AATCGCTCTGTGATCTGAGCTGAGAGACTCCTTGAGCTCAGAGCTCAGAAAGAAATGG 1200  
DB 2356 AATCGCTCTGTGATCTGAGCTGAGAGACTCCTTGAGCTCAGAGCTCAGAAAGAAATGG 2415  
QY 1201 AAGAGAAACCTAGCTTAACGAGAAATCTGAGAGGAGCAAGTGTTCCTCAGAGAAAGGG 1260  
DB 2416 AAGAGAAACCTAGCTTAACGAGAAATCTGAGAGGAGCAAGTGTTCCTCAGAGAAAGGG 2475  
QY 1261 GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGGCTGAGAGGAGTGGGAGAGCTGGGGC 1320  
DB 2476 GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGGCTGAGAGGAGTGGGAGAGCTGGGGC 2535  
QY 1321 TGAAGCGGTGTCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380  
DB 2536 TGAAGCGGTGTCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2595  
QY 1381 AGTGTGTTCACGAGGCTGGAGGATTTTCGTTGCTTCTGAGGCTTTTATCTTTTCT 1440  
DB 2596 AGTGTGTTCACGAGGCTGGAGGATTTTCGTTGCTTCTGAGGCTTTTATCTTTTCT 2655  
QY 1441 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAGGAGTCAAGTTTCAATAAGTCAAGCTGTT 1500  
DB 2656 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAGGAGTCAAGTTTCAATAAGTCAAGCTGTT 2715  
QY 1501 AAAATTCCAGGAGTGTGATGAGGTTTCTCTCAAGAGGCTTTAATTAAGGGAATATAG 1560  
DB 2716 AAAATTCCAGGAGTGTGATGAGGTTTCTCTCAAGAGGCTTTAATTAAGGGAATATAG 2775  
QY 1561 GAAGGAGCTAATTTCTAGGCGCTTAATTCACGAAAGAGTCAAGTCTTTTCTTT 1620  
DB 2776 GAAGGAGCTAATTTCTAGGCGCTTAATTCACGAAAGAGTCAAGTCTTTTCTTT 2835  
QY 1621 CATGTCTTCTGGGCACTACTCAGCCCTGTGTGTGATCTTGCTTAATGCAAGCGGTGCA 1680  
DB 2836 CATGTCTTCTGGGCACTACTCAGCCCTGTGTGTGATCTTGCTTAATGCAAGCGGTGCA 2895  
QY 1681 AACCTTGAATCAGAGAGCTGATTTCTTTCTGATTCAGCATGTTGGCTGTGCGAC 1740  
DB 2896 AACCTTGAATCAGAGAGCTGATTTCTTTCTGATTCAGCATGTTGGCTGTGCGAC 2955  
QY 1741 CGTGGGCAAGTGTCTCTCTTCTGAGGCAATAGTCTTCTGCTAATAAGACCTTGC 1800  
DB 2956 CGTGGGCAAGTGTCTCTCTTCTGAGGCAATAGTCTTCTGCTAATAAGACCTTGC 3015

Qy	1801	GCTCTCGTGTTCGTGAAACACTTCCCTGTGATATCTCTGTGTAAGGGGGGATCTTGAAGAGGG	1860
Db	3016	GCTCTCGTGTTCGTGAAACCTTCCCTGTGATATCTCTGAAGGGGGGATATTAAGAGGG	3075
Qy	1861	AAGGAGCCAGAGCTGAGAGCAGCTAGCAACAGGGGAGGTGAGGGGGGACAGGAAGCAGG	1920
Db	3076	AAGGAGCCAGAGCTGAGAGCAGCTAGCAACAGGGGAGGTGAGGGGGGACAGGAAGCAGG	3135
Qy	1921	CAGAAGCTGGGTGCTCATGACGTCTTCACTGATCAGCTCAGACTCCAGAACCGAGAGCCA	1980
Db	3136	CAGAAGCTGGGTGCTCATGACGTCTTCACTGATCAGACTCAGACTCCAGAACCGAGAGCCA	3195
Qy	1981	CAATGCTTCAGAAAGGCTCAATGAACCCCAACAGCCAACTTTTCCCTCCCTAAGCATAGAC	2040
Db	3196	CAATGCTTCAGAAAGGCTCAATGAACCCCAACAGCCAACTTTTCCCTCCCTAAGCATAGAC	3255
Qy	2041	AATGGCAATTTGSCAATATACCAAAAAAGATGACAGACCTAACTGGTGGTAGCTTTGGCTG	2100
Db	3256	AATGGCAATTTGSCAATATACCAAAAAAGATGACAGACCTAACTGGTGGTAGCTTTGGCTG	3315
Qy	2101	GCAATTCAAAACTGGGCGACAGCAAGTGGAAAAATGCCAGACATTTGTTAACTTTTCAACC	2160
Db	3316	GCAATTCAAAACTGGGCGACAGCAAGTGGAAAAATGCCAGACATTTGTTAACTTTTCAACC	3375
Qy	2161	TGACCAAGACCCCAACGACGCTCAGCAGTGACTGCTGACAGCACGAGTAGCTGACAGCC	2220
Db	3376	TGACCAAGACCCCAACGACGCTCAGCAGTGACTGCTGACAGCACGAGTAGCTGACAGCC	3435
Qy	2221	AGGGGAGGAGAAAAAGAGAGGAGTATGTATAGACAAAGAAACAGATTCATTCAG	2280
Db	3436	AGGGGAGGAGAAAAAGAGAGGAGTATGTATAGACAAAGAAACAGATTCATTCAG	3495
Qy	2281	GGCAGTGGGAATTGACACACAGGGAATTATAGTCCAGTATCTGGGTTCTTAGAGGACGG	2340
Db	3496	GGCAGTGGGAATTGACACACAGGGAATTATAGTCCAGTATCTGGGTTCTTAGAGGACGG	3555
Qy	2341	GCTATATTTGTGGGGGAAAAAATCAGTTCAGGGGAAGTCCGGGAACCTGATTTTATATAC	2400
Db	3556	GCTATATTTGTGGGGGAAAAAATCAGTTCAGGGGAAGTCCGGGAACCTGATTTTATATAC	3615
Qy	2401	TATATTTTCCCTTACAGAGTGAAGTAATTCGACCAAGTCAACAGGTATAGTAACTGAGGCT	2460
Db	3616	TATATTTTCCCTTACAGAGTGAAGTAATTCGACCAAGTCAACAGGTATAGTAACTGAGGCT	3675
Qy	2461	GTAAGATTAAGTATGTTCTCCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA	2520
Db	3676	GTAAGATTAAGTATGTTCTCCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA	3735
Qy	2521	AGGGCAATCCCGTTCTTTTAAACAGGAAGAAAACTTCTTAAGAGTAAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTCTTTTAAACAGGAAGAAAACTTCTTAAGAGTAAAGCCAAACAGAT	3795
Qy	2581	TCAAGCCCTAAGTCTTGCTGACATATATGATTTGTTTGAAGAAATCATTCCAGGAGGTT	2640
Db	3796	TCAAGCCCTAAGTCTTGCTGACATATATGATTTGTTTGAAGAAATCATTCCAGGAGGTT	3855
Qy	2641	TACTATCTGATTCAGAAAAATGACATAAGCTTTGGTCACTGATGAATTAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAAAATGACATAAGCTTTGGTCACTGATGAATTAACAAACCCAT	3915
Qy	2701	TTGTAAATGTCTCAAGTTCAAGGCTTAAGTCAGAAACCAATCAAAATAGAAATGAACTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAAGGCTTAAGTCAGAAACCAATCAAAATAGAAATGAACTTT	3975
Qy	2761	AGAGCAAACTGTGTTTCTTCCACTCTGAGAGTGAAGTCCACAGGGCAGTTTGGAAATATT	2820
Db	3976	AGAGCAAACTGTGTTTCTTCCACTCTGAGAGTGAAGTCCACAGGGCAGTTTGGAAATATT	4035
Qy	2821	ACTTCACAGTATTAAGCACTGTGTTGGATTAACAACATTAAGTTGCTCAAGAGCAATC	2880
Db	4036	ACTTCACAGTATTAAGCACTGTGTTGGATTAACAACATTAAGTTGCTCAAGAGCAATC	4095
Qy	2881	ATTATTTCAAGTGGCTTAAAGTTAATCTTGAACAGTTTGGTATATTTATTTGGCTATTGCC	2940

Db	4096	ATTATTTTCAAGGCTTAAGTACTTCGACAGTTTGTATATTTATTGCTATTGCG	4155
Qy	2941	ATTTCCTTTTGTGTTTTCTCTTGAGGTTTATTAATGTAAAGCAGGATTTTAACTTAC	3000
Db	4156	ATTTCCTTTTGTGTTTTCTCTTGAGGTTTATTAATGTAAAGCAGGATTTTAACTTAC	4215
Qy	3001	AGTCGAGAAAGCCTGTGAATTTGAAATGAGGAAAAATTCATTTTGTGTTTACACCTT	3060
Db	4216	AGTCGAGAAAGCCTGTGAATTTGAAATGAGGAAAAATTCATTTTGTGTTTACACCTT	4275
Qy	3061	CTAACCTAATTTTAACTATTTATTTCCATTGCGAATGAGCCATTAATCTCAAAGTGTAATA	3120
Db	4276	CTAACCTAATTTTAACTATTTATTTCCATTGCGAATGAGCCATTAATCTCAAAGTGTAATA	4335
Qy	3121	ACAGTACCTGTGATTTTGTCAATTACCAATAGAATTCAGACATTTTATATCTATATTACA	3180
Db	4336	ACAGTACCTGTGATTTTGTCAATTACCAATAGAATTCAGACATTTTATATCTATATTACA	4395
Qy	3181	GTTGTTCGAGATACGTTGTGAATGAAATTTTATATCTCAAAATCTATTGAAATTGACC	3240
Db	4396	GTTGTTCGAGATACGTTGTGAATGAAATTTTATATCTCAAAATCTATTGAAATTGACC	4455
Qy	3241	TCCGCTGGATCTTGTTTTTAAACATTAATTAATAACATGTTTAAATTTTGATATTGGA	3300
Db	4456	TCCGCTGGATCTTGTTTTTAAACATTAATTAATAACATGTTTAAATTTTGATATTGGA	4515
Qy	3301	TAAATCATATTTTCATTATCATATTTGTTTCTTTGTAAATCTATATTTTATATTGAAAA	3360
Db	4516	TAAATCATATTTTCATTATCATATTTGTTTCTTTGTAAATCTATATTTTATATTGAAAA	4575
Qy	3361	TCTTTTCTGAGAAAGTTCCTCCAGATTTTACCAATGAGTTCTTGGAATGCACACACG	3420
Db	4576	TCTTTTCTGAGAAAGTTCCTCCAGATTTTACCAATGAGTTCTTGGAATGCACACACG	4635
Qy	3421	AGTAAGAATCGATTTTGAAGGCTTAACATTAACAATGAGTGTGCTGAGATGCAAGA	3480
Db	4636	AGTAAGAATCGATTTTGAAGGCTTAACATTAACAATGAGTGTGCTGAGATGCAAGA	4695
Qy	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTTTAAAGCTAGGGTGAAGGGGAAATCTGC	3540
Db	4696	AGAAAGTTCTCCCAAGATACACAGTTGTTTTTAAAGCTAGGGTGAAGGGGAAATCTGC	4755
Qy	3541	CGCTTCTATAGGAATGCTCTCCCTGGAGCCTGTGAGGGTGTCTCTTGTGTTCTGGCTG	3600
Db	4756	CGCTTCTATAGGAATGCTCTCCCTGGAGCCTGTGAGGGTGTCTCTTGTGTTCTGGCTG	4815
Qy	3601	GCTGTATATTTTCTCTGTCCCTGTACTACGTTTAAAGACATGTTTGGATCTCCAGTTCC	3660
Db	4816	GCTGTATATTTTCTCTGTCCCTGTACTACGTTTAAAGACATGTTTGGATCTCCAGTTCC	4875
Qy	3661	AGCATAGTCCCTGACACAGTGCAGGTTCTCAATGATTTTGCAGAGTCAATGAAATATA	3720
Db	4876	AGCATAGTCCCTGACACAGTGCAGGTTCTCAATGATTTTGCAGAGTCAATGAAATATA	4935
Qy	3721	ACTAGAAATATATCTTGTGTAATCAGCACACAGTAATCTGTGTGTAATGTTGTGTAC	3780
Db	4936	ACTAGAAATATATCTTGTGTAATCAGCACACAGTAATCTGTGTGTAATGTTGTGTAC	4995
Qy	3781	--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3838
Db	4996	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5055
Qy	3839	GGGTATGGGNGCATTAATTTGGAGTGTCTTTTAAAAAGAAATCCAAACAGACTTCTGG	3898
Db	5056	GGGTATGGGNGCATTAATTTGGAGTGTCTTTTAAAAAGAAATCCAAACAGACTTCTGG	5115
Qy	3899	AAAGTATTTTCTTAAGAAATCTTGCTGGACAGCGTGAAGGCAACCCCTGTGCAAGCCCC	3958
Db	5116	AAAGTATTTTCTTAAGAAATCTTGCTGGACAGCGTGAAGGCAACCCCTGTGCAAGCCCC	5175
Qy	3959	ACCCAGCTCAGTGGCACCTGTGTCTTCCCAATGAAGGGCTGGCTCCCAATATATA	4018



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Db      5176 ACCGAGCCTCACTGCGCACCTGTGCTTCCGCCAGTAAGGGCTGCTCCCACTATATA 5235
QY      4019 TAAACCTCTCTGAGCTCAAGCATGAGCAGACGACCATTCAGGACCTTCAGC 4078
Db      5236 TAAACCTCTCTGAGCTCGGGCATGAGCAGACGACCATTCAGGACCTTCAGC 5295
QY      4079 ACAGC 4083
Db      5296 ACAGC 5300

RESULT 10
AAV51367
ID      AAV51367 standard; DNA; 5300 BP.
XX
AC      AAV51367;
XX
DT      27-OCT-1998 (first entry)
XX
DE      Human TIGR promoter variant TIGRv1 DNA.
XX
KM      TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KW      diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; sb.
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key
FT      mutation
FT      Location/Qualifiers
FT      /tag= a
FT      /note= "Wild-type A is replaced by G"
XX
XX      MO9832850-A1.
XX
XX      30-JUL-1998.
XX
XX      09-JAN-1998; 98MO-US000468.
XX
XX      28-JAN-1997; 97US-00791154.
XX      26-SEP-1997; 97US-00938669.
XX
XX      (REGC ) UNIV CALIFORNIA.
XX
XX      Nguyen TD, Polansky JR, Chen P, Chen H;
XX
XX      MPI; 1998-427946/36.
XX
XX      Use of TIGR nucleic acid sequences - used for, e.g. developing products
XX      for diagnosis, prognosis and treatment of glaucoma.
XX
XX      Disclosure; Fig 2; 105pp; English.
XX
XX      This sequence is a trabecular meshwork induced glucocorticoid response
XX      protein (TIGR) promoter variant, TIGRv1, which is used in a method for
XX      diagnosing glaucoma in a patient. The method involves the detection of
XX      polymorphisms whose presence is predictive of a mutation affecting TIGR
XX      response in the patient and can be diagnostic of glaucoma or steroid
XX      sensitivity. Base substitutions and base additions upstream of and within
XX      TIGR exons can also be used to diagnose glaucoma
XX
XX      Sequence 5300 BP; 1481 A; 1152 C; 1236 G; 1431 T; 0 U; 0 Other;
XX
Query Match      67.8%; Score 4067.8; DB 2; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
QY      1 GCTCCAGAGAACTCTCCCACTCTAGACTTTCGATCAAGATGTATACAGCCAGAAGCTC 60
Db      1216 GCTCCAGAGAACTCTCCCACTCTAGACTTTCGATCAAGATGTATACAGCCAGAAGCTC 1275
QY      61 CGTAGAGGTGAGGGTCTGTGTCTTACACCTGATGATGCTTACACCTGAGCTCACTGC 120
Db      1276 CGTAGAGGTGAGGGTCTGTGTCTTACACCTGATGATGCTTACACCTGAGCTCACTGC 1335

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QY      121 AACCTGACCTCCAGAGTTCAAGCAATTGTCCTGCTCAGCCCTCCGGAGCTGGGACT 180
Db      1336 AACCTGACCTCCAGAGTTCAAGCAATTGTCCTGCTCAGCCCTCCGGAGCTGGGACT 1395
QY      181 ACAGGCGCAGCCCGGCTAATTTTGTATGTGTAGTAGAGATGGGTTTCAACCATATTAG 240
Db      1396 ACAGGCGCAGCCCGGCTAATTTTGTATGTGTAGTAGAGATGGGTTTCAACCATATTAG 1455
QY      241 CCGGCTGGTCTTGAATCTCTGACCTCAGGTATCCACCACCTCAGCTCTTAAAGTGC 300
Db      1456 CCGGCTGGTCTTGAATCTCTGACCTCAGGTATCCACCACCTCAGCTCTTAAAGTGC 1515
QY      301 TGGGATTAAGGATGATGACCGGCGCGGCGCAAGGGTCAAGTTTAAATAGGAATAC 360
Db      1516 TGGGATTAAGGATGATGACCGGCGCGGCGCAAGGGTCAAGTTTAAATAGGAATAC 1575
QY      361 TTGAATGTTTACTAAACCAAGGAGGAAAGCAAAAGCTGTATTAATTCAGGAGATTC 420
Db      1576 TTGAATGTTTACTAAACCAAGGAGGAAAGCAAAAGCTGTATTAATTCAGGAGATTC 1635
QY      421 TTGGGATGGGGAATGTGTGCTAGAGCTGCTGTGCTAGTCCAGACCACTGTGCTCATCA 480
Db      1636 TTGGGATGGGGAATGTGTGCTAGAGCTGCTGTGCTAGTCCAGACCACTGTGCTCATCA 1695
QY      481 CTTTCTTCCCTCATCTCATTTTTCAGGGCTAAGTTACATTTTATTCACATGCTTTTGTG 540
Db      1696 CTTTCTTCCCTCATCTCATTTTTCAGGGCTAAGTTACATTTTATTCACATGCTTTTGTG 1755
QY      541 GTAAGCCTTCACATGCTTACTGAAATTAAGATATACATTAACCTAGTTCATTGGGGCCA 600
Db      1756 GTAAGCCTTCACATGCTTACTGAAATTAAGATATACATTAACCTAGTTCATTGGGGCCA 1815
QY      601 TCTGTGTGTGTATAGGGAGAGGGCATACCCAGAGACTCTTGAAGCCCGGCGAG 660
Db      1816 TCTGTGTGTGTATAGGGAGAGGGCATACCCAGAGACTCTTGAAGCCCGGCGAG 1875
QY      661 AGGTTTCTCTCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCTCTGGGTGCTCGAGCA 720
Db      1876 AGGTTTCTCTCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCTCTGGGTGCTCGAGCA 1935
QY      721 ACCTCGACGCCGTGCCACTGTGTTGTTTGTATCACTCTTAGGGAACCTGTGCTTCT 780
Db      1936 ACCTCGACGCCGTGCCACTGTGTTGTTTGTATCACTCTTAGGGAACCTGTGCTTCT 1995
QY      781 ATTTCTGTGTGACTGCTGTTCAATTCACAGGACATTCAGCAATTTATTTAGTACTTATA 840
Db      1996 ATTTCTGTGTGACTGCTGTTCAATTCACAGGACATTCAGCAATTTATTTAGTACTTATA 2055
QY      841 TCTGCCAGACACCAAGACAAATGTGTAGCAAAAGCATGTCCTGCTTCTGTTGAG 900
Db      2056 TCTGCCAGACACCAAGACAAATGTGTAGCAAAAGCATGTCCTGCTTCTGTTGAG 2115
QY      901 GTGACAGTTTCTCATGAGAAAGGTGACAGAAATTAATATAGCCAGCAATTAACCCA 960
Db      2116 GTGACAGTTTCTCATGAGAAAGGTGACAGAAATTAATATAGCCAGCAATTAACCCA 2175
QY      961 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGAAATTTGCGGAGCATTCCTTAACA 1020
Db      2176 GTGCTGAAAGAAAGAAATTAACACCATCTTGAAGAAATTTGCGGAGCATTCCTTAACA 2235
QY      1021 GGGCACTCCCTAGAGGCCCCCTGCTGCTCAATGTCGCCGAGGCCCCCAAGCCCGAGT 1080
Db      2236 GGGCACTCCCTAGAGGCCCCCTGCTGCTCAATGTCGCCGAGGCCCCCAAGCCCGAGT 2295
QY      1081 CTTCAAGCTCTCTCTCATCATGTCACAGGCTGCACTGGCTGCTGCTTCCGCTG 1140
Db      2296 CTTCAAGCTCTCTCTCATCATGTCACAGGCTGCACTGGCTGCTGCTTCCGCTG 2355
QY      1141 AATGCTCTGTGTGATCTGAGCTGGAAGACTCTTGTGCTCCAGGCTCCAGAAAGAAATGG 1200
Db      2356 AATGCTCTGTGTGATCTGAGCTGGAAGACTCTTGTGCTCCAGGCTCCAGAAAGAAATGG 2415

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QY	1201	AGAGGAGAACTAAGCTTAACGGAGATCTGGAGGGGACAAGTCTTCTCAGAGGAAAGG	1260
Db	2416	AGAGGAGAACTAAGCTTAACGGAGATCTGGAGGGGACAAGTCTTCTCAGAGGAAAGG	2475
QY	1261	GCTCCACAGTCCAGAGAGATTCCAGAGAGTGGGACCTGCAGAGAGTGGGACGCTGGAGG	1320
Db	2476	GCTCCACAGTCCAGAGAGATTCCAGAGAGTGGGACCTGCAGAGAGTGGGACGCTGGAGG	2535
QY	1321	TGAGCGGCTGCTGAAAGGCAGAGAGGTGAAAAGGACAGCTGAAGCTGCCAGATGTC	1380
Db	2536	TGAGCGGCTGCTGAAAGGCAGAGAGGTGAAAAGGACAGCTGAAGCTGCCAGATGTC	2595
QY	1381	AGTGTGTTCAAGGGGCTGGGAGTCTCCGTGCTCTGAGACCTTTTATCTTTTCT	1440
Db	2596	AGTGTGTTCAAGGGGCTGGGAGTCTCCGTGCTCTGAGACCTTTTATCTTTTCT	2655
QY	1441	CTGCTGGAGAGAGAAAGTCTATTCTATGAAAGGATGCAAGTTCATAAAGTCAGCTGT	1500
Db	2656	CTGCTGGAGAGAGAAAGTCTATTCTATGAAAGGATGCAAGTTCATAAAGTCAGCTGT	2715
QY	1501	AAAAATCCAGGGTGTGATGGGTTTCTTCACAGAGGCTTTTATTTAATGGAAATAG	1560
Db	2716	AAAAATCCAGGGTGTGATGGGTTTCTTCACAGAGGCTTTTATTTAATGGAAATAG	2775
QY	1561	GAAGCGAGCTATTTCTTAAGCCGTTAATTAACAGAAAGATGACTGAAGCTTTCTTT	1620
Db	2776	GAAGCGAGCTATTTCTTAAGCCGTTAATTAACAGAAAGATGACTGAAGCTTTCTTT	2835
QY	1621	CATGCTCTGAGGCACTACTCAGCCCTGTGTGTGACTGGCTATATCAGAAGGCTGAA	1680
Db	2836	CATGCTCTGAGGCACTACTCAGCCCTGTGTGTGACTGGCTATATCAGAAGGCTGAA	2895
QY	1681	AACCTTGGAACTCAGAGAGCTGGTTTCTTTCTGATTCTGCATTTGGTGTGTGCGAC	1740
Db	2896	AACCTTGGAACTCAGAGAGCTGGTTTCTTTCTGATTCTGCATTTGGTGTGTGCGAC	2955
QY	1741	CGTGGGCAAGTGTCTCTCTCTTCCTGGGCAATAGCTTTCTCTGCTATPAAAGCCCTTGCA	1800
Db	2956	CGTGGGCAAGTGTCTCTCTCTTCCTGGGCAATAGCTTTCTCTGCTATPAAAGCCCTTGCA	3015
QY	1801	GCTCTCGGTTCTGTGAACTATCCCTGTGATCTCTGTGAGGGGGATGTGTAGAGGGG	1860
Db	3016	GCTCTCGGTTCTGTGAACTATCCCTGTGATCTCTGTGAGGGGGATGTGTAGAGGGG	3075
QY	1861	AAGAGGCGAGCTGGAGCACTGAGCCAGCCAGGGGAGGTGAGGGGGACAGAGAGCGAGG	1920
Db	3076	AAGAGGCGAGCTGGAGCACTGAGCCAGCCAGGGGAGGTGAGGGGGACAGAGAGCGAGG	3135
QY	1921	CAGAAAGCTGGTGCTCCATCACTAGCTCTCACTATCACTCAGATCCAGAACCGAGACCA	1980
Db	3136	CAGAAAGCTGGTGCTCCATCACTAGCTCTCACTATCACTCAGAACCGAGAACCA	3195
QY	1981	CAATGCTCAGGAAAGCTCAATGAAACCAACAGCCCAATTTCTCTCCCTTAAGATAGAC	2040
Db	3196	CAATGCTCAGGAAAGCTCAATGAAACCAACAGCCCAATTTCTCTCCCTTAAGATAGAC	3255
QY	2041	AATGCAATTTGCCATTAACCAAAAAGATGACAGACTTAACCTGGTGTAGCTTTTGCTG	2100
Db	3256	AATGCAATTTGCCATTAACCAAAAAGATGACAGACTTAACCTGGTGTAGCTTTTGCTG	3315
QY	2101	GCATTCAAAAATGAGGCGACAGCAAGTGGAAAATGCCAGAGATTGTAACTTTTCAACC	2160
Db	3316	GCATTCAAAAATGAGGCGACAGCAAGTGGAAAATGCCAGAGATTGTAACTTTTCAACC	3375
QY	2161	TGACCAAGCAACCCACAGCAAGCTTACAGATGATCTGCTGACACACGAGTGAACCTGACGC	2220
Db	3376	TGACCAAGCAACCCACAGCAAGCTTACAGATGATCTGCTGACACACGAGTGAACCTGACGC	3435
QY	2221	AGGGAGGAGAAAGAAAAGAGGAGATGTGTATGACAGAAAGACAGATTCACTTCAAG	2280
Db	3436	AGGGAGGAGAAAGAAAAGAGGAGATGTGTATGACAGAAAGACAGATTCACTTCAAG	3495
QY	2281	GGCAGTGGGAATTGACACAGGGATTAATAGTCCAGTATCCTGGGTTCTAGAGCGAGG	2340

Db	3496	GGCAATGGGAATTGACACAGGGAATTATAGTCCAGTGAATCTGGGTTCTAGAGGCAAG	3555
Qy	2341	GCTATATTTGTGGGGGAAAAAATCAAGTTCAGGGAAGTGGGAGACTGATTTCTAATAC	2400
Db	3556	GCTATATTTGTGGGGGAAAAAATCAAGTTCAGGGAAGTGGGAGACTGATTTCTAATAC	3615
Qy	2401	TATATTTTTCCTTTACAGCTGAGTAATCTCGACAGTCAAGGTAAGTAAGGCT	2460
Db	3616	TATATTTTTCCTTTACAGCTGAGTAATCTGAGCAAGTCAAGGTAAGTAAGGCT	3675
Qy	2461	GTAAATTAAGTAAAGTTCCTTTTAAAGGACCTCTTTCTCTGTGAGTTAGCAGACA	2520
Db	3676	GTAAATTAAGTAAAGTTCCTTTTAAAGGACCTCTTTCTCTGTGAGTTAGCAGACA	3735
Qy	2521	AGGGCAATCCCGTTTCCTTTTACAGAAAGAAAAATCTTAAGAGTAAAGCCAAAGAT	2580
Db	3736	AGGGCAATCCCGTTTCCTTTTACAGAAAGAAAAATCTTAAGAGTAAAGCCAAAGAT	3795
Qy	2581	TCAAGCCTAAGGCTTGTCTGACTATATGATGGTTTTGAAAAATCATTTCAAGCATGTT	2640
Db	3796	TCAAGCCTAAGGCTTGTCTGACTATATGATGGTTTTGAAAAATCATTTCAAGCATGTT	3855
Qy	2641	TACTATCTGATTCAGAAAAAGAGACTAGTAACTGTAACCTTGGTCAAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAAAAGAGACTAGTAACTGTAACCTTGGTCAAGCTGTAAACAAACCCAT	3915
Qy	2701	TTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAAACCAATCAATTAAGATAGATCTTT	2760
Db	3916	TTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAAACCAATCAATTAAGATAGATCTTT	3975
Qy	2761	AGAGCAAACTGTGTTTCTCCACTCTGGAGGTGAGTCTGCCAAGGCACTTTGGAATATTT	2820
Db	3976	AGAGCAAACTGTGTTTCTCCACTCTGGAGGTGAGTCTGCCAAGGCACTTTGGAATATTT	4035
Qy	2821	ACTTCACAGTATTAACACTGTGTTGTTGTAATTAACAACATTAAGTGTCAAAAGGCAATC	2880
Db	4036	ACTTCACAGTATTAACACTGTGTTGTTGTAATTAACAACATTAAGTGTCTAAAGGCAATC	4095
Qy	2881	ATTATTTCAAGTGGCTTAAGTTACTCTGACAGTTTGGTATTTATTTGGCTATTTGCC	2940
Db	4096	ATTATTTCAAGTGGCTTAAGTTACTCTGACAGTTTGGTATTTATTTGGCTATTTGCC	4155
Qy	2941	ATTGCTTTTGTGTTTTCTCTTTGGGTTTATTAATGTAAGACAGGATTTAACTTAC	3000
Db	4156	ATTGCTTTTGTGTTTTCTCTTTGGGTTTATTAATGTAAGACAGGATTTAACTTAC	4215
Qy	3001	AGTCCAGAAAGCCTGGAATTTGAATGAGAAAAATTAATCATTTTGTTTTACCACTT	3060
Db	4216	AGTCCAGAAAGCCTGGAATTTGAATGAGAAAAATTAATCATTTTGTTTTACCACTT	4275
Qy	3061	CTAATCAATTTAAACATTTTATTCATTCGAAATAGAGCATTAACATCAAGTGTATATA	3120
Db	4276	CTAATCAATTTAAACATTTTATTCATTCGAAATAGAGCATTAACATCAAGTGTATATA	4335
Qy	3121	ACAGTACCTGATTTTGTCAATTAACCAATAGAATCAAGACATTTTATATCTATTTACA	3180
Db	4336	ACAGTACCTGATTTTGTCAATTAACCAATAGAATCAAGACATTTTATCTATTTACA	4395
Qy	3181	GTGTTGTCAGATACGTTGTAAGTGAATTTTATCTCAAAACTACTTTGAATTAGACC	3240
Db	4396	GTGTTGTCAGATACGTTGTAAGTGAATTTTATCTCAAAACTACTTTGAAATTAGACC	4455
Qy	3241	TCTGTGTGATCTGTGTTTAAACATTAATTAACATGTTTAAATTTTGATATTTTGA	3300
Db	4456	TCTGTGTGATCTGTGTTTAAACATTAATTAACATGTTTAAATTTTGATATTTTGA	4515
Qy	3301	TATCATATTTCAATTAATCTGTTGTTCTTGTGAATCTATATTTTATATTTGAAAAACA	3360
Db	4516	TATCATATTTCAATTAATCTGTTGTTCTTGTGAATCTATATTTTATATTTGAAAAACA	4575
Qy	3361	TCCTTTCTGAGAAAGTTCCTCCAGATTTTACCAATGAGGTTCTTGGCATGCAACACAG	3420

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Db      4576 TCTTTCTGAGAGAGATTCCCCAGATTTCCACCAATGAGTTCTTGGCATGCACACACAG 4635
Qy      3421 AGTAAAGAACTGATTAGAGGCTAAACATTGACATTGTGCTCGAGATGCAAGACTGAATT 3480
Db      4636 AGTAAAGAACTGATTAGAGGCTAAACATTGACATTGTGCTCGAGATGCAAGACTGAATT 4695
Qy      3481 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGGGGAAATCTGC 3540
Db      4696 AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAGAGGCTGAGGGGAAATCTGC 4755
Qy      3541 CGCTCTAATAGGAATGCTCCCTCGAGAGCTGAGAGGCTGCTGCTTGTGTTCTGCTG 3600
Db      4756 CGCTCTAATAGGAATGCTCCCTCGAGAGCTGAGAGGCTGCTGCTTGTGTTCTGCTG 4815
Qy      3601 GCTGTTATTTTCTCTGCTCCCTGCTAGCTCTTAAAGAACTGTTGATCTCCAGTTCT 3660
Db      4816 GCTGTTATTTTCTCTGCTCCCTGCTAGCTCTTAAAGAACTGTTGATCTCCAGTTCT 4875
Qy      3661 AGCATAGTGCCTGGCAGATGCAAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATA 3720
Db      4876 AGCATAGTGCCTGGCAGATGCAAGTTCTCAATGAGTTTGCAGAGTGAATGGAATATA 4935
Qy      3721 ACTAGAAATATATCTCTGTTGAATACGACACCAAGTCTGCTGCTGTAAGTGTGTAC 3780
Db      4936 ACTAGAAATATATCTCTGTTGAATACGACACCAAGTCTGCTGCTGTAAGTGTGTAC 4995
Qy      3781 --GTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3838
Db      4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5055
Qy      3839 GGGTATGAGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGG 3898
Db      5056 GGGTATGAGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGG 5115
Qy      3899 AAGTATTTTCTTAAGATTTTGTGTGACGCTGAGGAGCAACCCCTGTGCAACGCCC 3958
Db      5116 AAGTATTTTCTTAAGATTTTGTGTGACGCTGAGGAGCAACCCCTGTGCAACGCCC 5175
Qy      3959 ACCAGGCTCAGGAGGCACTCTGCTTCCCATGAAGAGGCTGCTCCCATGATATA 4018
Db      5176 ACCAGGCTCAGGAGGCACTCTGCTTCCCATGAAGAGGCTGCTCCCATGATATA 5235
Qy      4019 TAAACCTCTGTGAGCTCAGAGCATGAGCCAGCAAGGCAACCCATCCAGGCACTCTCAG 4078
Db      5236 TAAACCTCTGTGAGCTCAGAGCATGAGCCAGCAAGGCAACCCATCCAGGCACTCTCAG 5295
Qy      4079 ACAGC 4083
Db      5296 ACAGC 5300

RESULT 11
ID      AAV51363 standard; DNA; 5300 BP.
AC      AAV51363;
XX      27-OCT-1998 (first entry)
DE      Human TIGR promoter mutant TIGRmt2 DNA.
XX      TIGR; trabecular meshwork induced glucocorticoid response protein; human;
KM      diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.
XX      Homo sapiens.
OS      Synthetic.
XX      Key
FH      Location/Qualifiers
FT      mutation
FT      /tag= a
FT      /note= "wild-type C is replaced with T"
PN      WO9832850-A1.

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XX      30-JUL-1998.
PD      09-JAN-1998; 98MO-US000468.
XX      28-JAN-1997; 97US-00791154.
PR      26-SEP-1997; 97US-00938669.
XX      (REGC ) UNIV CALIFORNIA.
XX      Nguyen TD, Polansky JR, Chen P, Chen H;
PI      WPI; 1998-427946/36.
XX      Use of TIGR nucleic acid sequences - used for, e.g. developing products
PT      for diagnosis, prognosis and treatment of glaucoma.
XX      Disclosure; Fig 2; 105pp; English.
PS      This sequence is a trabecular meshwork induced glucocorticoid response
CC      protein (TIGR) promoter mutant, TIGRmt2, which is used in a method for
CC      diagnosing glaucoma in a patient. The method involves the detection of
CC      polymorphisms whose presence is predictive of a mutation affecting TIGR
CC      response in the patient and can be diagnostic of glaucoma or steroid
CC      sensitivity. Base substitutions and base additions upstream of and within
CC      TIGR exons can also be used to diagnose glaucoma
SQ      Sequence 5300 BP; 1482 A; 1151 C; 1235 G; 1432 T; 0 U; 0 Other;
Query Match 67.8%; Score 4067.8; DB 2; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
Qy      1 GCTCCACAGGAAGTCTCCCACTTGAAGCTTGTGATCATGATGATGTTACAGCAGAGCTC 60
Db      1216 GCTCCACAGGAAGTCTCCCACTTGAAGCTTGTGATCATGATGATGTTACAGCAGAGCTC 1275
Qy      61 CGTGAAGGATGAGGCTGTGTGTTTACCTACCTATGCTTACACCTGAGCTCACTGC 120
Db      1276 CGTGAAGGATGAGGCTGTGTGTTTACCTACCTATGCTTACACCTGAGCTCACTGC 1335
Qy      121 AACTCTGCTCCCAAGTTCAGCAATTCCTGCTGCTGAGCTCCCGGTAGCTGGAGT 180
Db      1336 AACTCTGCTCCCAAGTTCAGCAATTCCTGCTGCTGAGCTCCCGGTAGCTGGAGT 1395
Qy      181 AAGGCGCAGCGCCGCTAATTTTGTATTTGTAGTGAAGATGGGTTTACCATATTTAG 240
Db      1396 AAGGCGCAGCGCCGCTAATTTTGTATTTGTAGTGAAGATGGGTTTACCATATTTAG 1455
Qy      241 CCGGCTGCTCTTGAATCTCTGACCTCAGGTGATCCACCCACTGAGCTCTTAAGTTC 300
Db      1456 CCGGCTGCTCTTGAATCTCTGACCTCAGGTGATCCACCCACTGAGCTCTTAAGTTC 1515
Qy      301 TGGGATTAAGGATGATGATCAGCGCGCGGCAAGGCTGATGTTTATAAGATTAAC 360
Db      1516 TGGGATTAAGGATGATGATCAGCGCGCGGCAAGGCTGATGTTTATAAGATTAAC 1575
Qy      361 TTGAATGTTTACTTAACCAACAGGAAACAGCAAAAGCTGTGATTAATTTCAAGGATTC 420
Db      1576 TTGAATGTTTACTTAACCAACAGGAAACAGCAAAAGCTGTGATTAATTTCAAGGATTC 1635
Qy      421 TTGGATGAGGAAATGTGCTCATGAGTCTGCTGCTGCTCCAGACACTGCTCATCA 480
Db      1636 TTGGATGAGGAAATGTGCTCATGAGTCTGCTGCTGCTCCAGACACTGCTCATCA 1695
Qy      481 CTTTCTTCCCTCATCTCATTTTTCAGGCTAAGTATCAATTTTATTTACCATGCTTTTGG 540
Db      1696 CTTTCTTCCCTCATCTCATTTTTCAGGCTAAGTATCAATTTTATTTACCATGCTTTTGG 1755
Qy      541 GTAGCTTCACATGTTTACGAAATTAAGATTAACATTAACATGATTCATTTGGGGCCA 600
Db      1756 GTAGCTTCACATGTTTACGAAATTAAGATTAACATTAACATGATTCATTTGGGGCCA 1815

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QY 601 TCTGTGTGTGTATAGGGAGAGAGGAGATACCCAGAGACTCTTTGAAGCCCCGGGAG 660  
 DB 1816 TCTGTGTGTGTATAGGGAGAGAGGAGATACCCAGAGACTCTTTGAAGCCCCGGGAG 1875  
 QY 661 AGGTTTCTCTCCAGCTGGGGAGCCCTTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 720  
 DB 1876 AGGTTTCTCTCCAGCTGGGGAGCCCTTGCAAGCACCCGGGGTCTGGGTGTCTGAGCA 1935  
 QY 721 ACCTGCAAGCCCGTGCACCTGGTGTGTTTGTATGACTCTCTAGAGGACCTGTGTCTTCT 780  
 DB 1936 ACCTGCAAGCCCGTGCACCTGGTGTGTTTGTATGACTCTCTAGAGGACCTGTGTCTTCT 1995  
 QY 781 ATTTCTGTGTGACTGTTCAATTCATCCAGGACATTCATTGACAAATTTATTAAGTACTTATA 840  
 DB 1996 ATTTCTGTGTGACTGTTCAATTCATCCAGGACATTCATTGACAAATTTATTAAGTACTTATA 2055  
 QY 841 TTGCGCAGACACCAAGACAAATAGTGAGCAAGACATCTGCCCCCTTACCTTGTGGAG 900  
 DB 2056 TTGCGCAGACACCAAGACAAATAGTGAGCAAGACATCTGCCCCCTTACCTTGTGGAG 2115  
 QY 901 GTGACAGTTTCTCATGGAAGAGTGCAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 960  
 DB 2116 GTGACAGTTTCTCATGGAAGAGTGCAGAAAGAAATTAATAGCCAGCCAACTTAAACCA 2175  
 QY 961 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAAACA 1020  
 DB 2176 GTGCTGAAGAAAGAAATTAACACCATCTTGAAGATTTGTGCGAGCATCCCTTAAACA 2235  
 QY 1021 GGGCACCCTCCCTAGAGCCCCCTGTCTCTCATCTGTGCCCCGAGGCCCCAGCCGAGT 1080  
 DB 2236 GGGCACCCTCCCTAGAGCCCCCTGTCTCTCATCTGTGCCCCGAGGCCCCAGCCGAGT 2295  
 QY 1081 CTTCCAAAGCCTCCTCCTCATGATCAGACAGCTGAGCTGAGCTGCTCGCTTCCCGTG 1140  
 DB 2296 CTTCCAAAGCCTCCTCCTCATGATCAGACAGCTGAGCTGAGCTGCTCGCTTCCCGTG 2355  
 QY 1141 AATGCTCTGTGTGATCTGAGCTGAGAGCTCTTGTGCTCAGGCTTCAGAAAGAAATAG 1200  
 DB 2356 AATGCTCTGTGTGATCTGAGCTGAGAGCTCTTGTGCTCAGGCTTCAGAAAGAAATAG 2415  
 QY 1201 AAGAGGAAACTAGTCTTAACGGAGAACTGTGAGGGGACATGTGTTTCTCAGAGGAAAGG 1260  
 DB 2416 AAGAGGAAACTAGTCTTAACGGAGAACTGTGAGGGGACATGTGTTTCTCAGAGGAAAGG 2475  
 QY 1261 GCCTCCAGCTCAGAGGAAATTCAGAGGCTGGGAGCTGAGGAGATGGGGAGCGCTGGGAC 1320  
 DB 2476 GCCTCCAGCTCAGAGGAAATTCAGAGGCTGGGAGCTGAGGAGATGGGGAGCGCTGGGAC 2535  
 QY 1321 TGAGCGGCTGTGAAGGAGAGAGTGAAGAGGCGAGGCTGAAAGCTGCCAGATGTTTC 1380  
 DB 2536 TGAGCGGCTGTGAAGGAGAGAGTGAAGAGGCGAGGCTGAAAGCTGCCAGATGTTTC 2595  
 QY 1381 AGTGTGTGTCAAGGGCTGGGAGTTTCCGTGCTCTGTGAGCTTTTATCTTTTCT 1440  
 DB 2596 AGTGTGTGTCAAGGGCTGGGAGTTTCCGTGCTCTGTGAGCTTTTATCTTTTCT 2655  
 QY 1441 CTGCTTGAAGAGAAAGTCTATTTCATGAAGGATGCAAGTTTCAATAAGTCAAGCTGT 1500  
 DB 2656 CTGCTTGAAGAGAAAGTCTATTTCATGAAGGATGCAAGTTTCAATAAGTCAAGCTGT 2715  
 QY 1501 AAAATTCAGAGGTGTGCATGGTGTCTTCAAGAAAGCTTTTATTTAAATGGGAATATAG 1560  
 DB 2716 AAAATTCAGAGGTGTGCATGGTGTCTTCAAGAAAGCTTTTATTTAAATGGGAATATAG 2775  
 QY 1561 GAAAGCAGCTCATTTTCTTAGGCGGTAAATTCAGGAAAGATGACTGTGAGTCTTTTCTT 1620  
 DB 2776 GAAAGCAGCTCATTTTCTTAGGCGGTAAATTCAGGAAAGATGACTGTGAGTCTTTTCTT 2835  
 QY 1621 CATGTCTTGGGCACTACTCAGCCCTGTGTGAGCTTGCTTATGCAAGAGCGTGCAG 1680  
 DB 2836 CATGTCTTGGGCACTACTCAGCCCTGTGTGAGCTTGCTTATGCAAGAGCGTGCAG 2895  
 QY 1681 AACCTTGAATCAGAGACTCGGTTTCTTCTGTGTTCTGCCATTGGGTGGCTGTGCAG 1740

DB 2896 AACCTTGAATCAGAGACTCGGTTTCTTCTGTGTTCTGCATTTGGCTGTGTGCAGC 2955  
 QY 1741 CGTGGGCAAGTGTCTCTCTCCCTGGGCCATAGTCTTCTGTGTAATAAGACCTTGCA 1800  
 DB 2956 CGTGGGCAAGTGTCTCTCTCCCTGGGCCATAGTCTTCTGTGTAATAAGACCTTGCA 3015  
 QY 1801 GCTCTGTGTGTGTGAAACAATTCCTGTGATTTCTGTGAGGGGAGATGTTGAGAGGG 1860  
 DB 3016 GCTCTGTGTGTGTGAAACAATTCCTGTGATTTCTGTGAGGGGAGATGTTGAGAGGG 3075  
 QY 1861 AAGAGGCAAGCTGTGAGAGCTGAGCCACAGGGGAGGTGAGGGGAGCAGAAAGCCAGG 1920  
 DB 3076 AAGAGGCAAGCTGTGAGAGCTGAGCCACAGGGGAGGTGAGGGGAGCAGAAAGCCAGG 3135  
 QY 1921 CAGAAAGCTGGGTGCATCAGTCACTGATGATCAGCTGAGACTCCAGAGCCGAGGCCA 1980  
 DB 3136 CAGAAAGCTGGGTGCATCAGTCACTGATGATCAGCTGAGACTCCAGAGCCGAGGCCA 3195  
 QY 1981 CAATGCTTCAGAAAGCTCAATGAACCAACCAAGCCCAATTTCTTCCCTAAGCATAGAC 2040  
 DB 3196 CAATGCTTCAGAAAGCTCAATGAACCAACCAAGCCCAATTTCTTCCCTAAGCATAGAC 3255  
 QY 2041 AATGCAATTTGCCAATTAACCAAAAGAAATGCAAGACTAACTGGTGTAGCTTTTGCTG 2100  
 DB 3256 AATGCAATTTGCCAATTAACCAAAAGAAATGCAAGACTAACTGGTGTAGCTTTTGCTG 3315  
 QY 2101 GCATTCAAAAACCTGGGCGAGAGCAAGTGAATAATGCGAGAGATTGTTAACTTTTCAACC 2160  
 DB 3316 GCATTCAAAAACCTGGGCGAGAGCAAGTGAATAATGCGAGAGATTGTTAACTTTTCAACC 3375  
 QY 2161 TGACCAAGCACCACAGCAGCTCAGCAGTACTGTGACAGAGCGAGTGAACCTGACGGC 2220  
 DB 3376 TGACCAAGCACCACAGCAGCTCAGCAGTACTGTGACAGAGCGAGTGAACCTGACGGC 3435  
 QY 2221 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCAATTGACAG 2280  
 DB 3436 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCAATTGACAG 3495  
 QY 2281 GGCAGTGGGAATTGACCAAGAGATTAATAGTCAAGTATCTGGGTTCTAGAGAGCCAGG 2340  
 DB 3496 GGCAGTGGGAATTGACCAAGAGATTAATAGTCAAGTATCTGGGTTCTAGAGAGCCAGG 3555  
 QY 2341 GCTATATTGTGGGGGAAAAAATCAATTCAAGGAGAGTGGGAGACCTGATTTCTAATAC 2400  
 DB 3556 GCTATATTGTGGGGGAAAAAATCAATTCAAGGAGAGTGGGAGACCTGATTTCTAATAC 3615  
 QY 2401 TATATTTTCTTTTACAAAGCTGATTAATCTGAGCAATCAAGTATGTAAGTGAAGCT 2460  
 DB 3616 TATATTTTCTTTTACAAAGCTGATTAATCTGAGCAATCAAGTATGTAAGTGAAGCT 3675  
 QY 2461 GTAAGTACTTAGTTTCTCCCTAATTAGGAATCTTTTCTCTGTGAGTTAGCAGACA 2520  
 DB 3676 GTAAGTACTTAGTTTCTCCCTAATTAGGAATCTTTTCTCTGTGAGTTAGCAGACA 3735  
 QY 2521 AGGGCAATCCGTTTCTTTTAAACAGAGAAACAATTCCTAAGAGTAAAGCCAAAGAT 2580  
 DB 3736 AGGGCAATCCGTTTCTTTTAAACAGAGAAACAATTCCTAAGAGTAAAGCCAAAGAT 3795  
 QY 2581 TCAAGCTAGAGCTTGTGCTGAGCTATATGATGGTGTGTTTGAAGAAATCATTTCAAGCA 2640  
 DB 3796 TCAAGCTAGAGCTTGTGCTGAGCTATATGATGGTGTGTTTGAAGAAATCATTTCAAGCA 3855  
 QY 2641 TACTATCTGAATCAGAAATGAGACTAGTACCTTTGTGCTGAGCTGTAACAAACACCAT 2700  
 DB 3856 TACTATCTGAATCAGAAATGAGACTAGTACCTTTGTGCTGAGCTGTAACAAACACCAT 3915  
 QY 2701 TTGTAATGTCTCAAGTTCAAGCTTAATCTGCAAGCAACATCAATTAAGATTAAGATCTTT 2760  
 DB 3916 TTGTAATGTCTCAAGTTCAAGCTTAATCTGCAAGCAACATCAATTAAGATTAAGATCTTT 3975  
 QY 2761 AAGCAAACTGTGTTTCTCAGCTGTGAGGTGAGTCTGACAGGGAGTTTGAATAATTT 2820

ID	Sequence	Location/Qualifiers
QY	3899 AAGGTATTTTCTCAAGAAATCTGTGCTGAGGCTGAAGGCAACCCCCCTGTGCACAGCCCC	
Db	5116 AAGGTTATTTTCTTAGAAATCTTCTGTCGCAAGCTTAAGGCAACCCCCCTGTGCACAGCCCC	
QY	3959 ACCGAGCTCAGCTGAGCCACCTCTGTCTTCCCCCATGAAGGAGCTGAGCTCCCCAGTATATA	
Db	5176 ACCGAGCTCAGCTGAGCCACCTCTGTCTTCCCCCATGAAGGAGCTGAGCTCCCCAGTATATA	
QY	4019 TAAACCTCTCTGAGGCTCAGGCGATGAGCGAAGGCGCAACCATTCAGGCACTCTCAGC	
Db	5236 TAAACCTCTCTGAGGCTCAGGCGATGAGCGAAGGCGCAACCATTCAGGCACTCTCAGC	
QY	4079 ACAGC 4083	
Db	5296 ACAGC 5300	
RESULT 12		
ID	AAVS1366	AAVS1366 standard; DNA; 5300 BP.
XX	AAVS1366;	
DT	27-OCT-1998	(first entry)
DE	Human TIGR promoter mutant TIGRmt5 DNA.	
XX		
KX	TIGR; trabecular meshwork induced glucocorticoid response protein; human;	
KW	diagnosis; glaucoma; polymorphism; steroid sensitivity; mutant; ss.	
XX		
OS	Homo sapiens.	
XX	Synthetic.	
FX	Key	Location/Qualifiers
FT	mutation	4262
FT	/*tag= a	/note= "wild-type G is replaced with A"
PN	W09832850-A1.	
XX	30-JUL-1998.	
PD	XX	
PF	09-JUN-1998;	98WO-US000468.
XX	28-JAN-1997;	97US-00791154.
XX	26-SEP-1997;	97US-00938669.
XX	(REGC ) UNIV CALIFORNIA.	
XX	Nguyen TD, Polansky JR, Chen P, Chen H;	
XX	WPI; 1998-427946/36.	
XX	Use of TIGR nucleic acid sequences - used for, e.g. developing products	
XX	for diagnosis, prognosis and treatment of glaucoma.	
XX	Disclosure; Fig 2; 105pp; English.	
CC	This sequence is a trabecular meshwork induced glucocorticoid response	
CC	protein (TIGR) promoter mutant, TIGRmt5, which is used in a method for	
CC	diagnosing glaucoma in a patient. The method involves the detection of	
CC	polymorphisms whose presence is predictive of a mutation affecting TIGR	
CC	response in the patient and can be diagnostic of glaucoma or steroid	
CC	sensitivity. Base substitutions and base additions upstream of and within	
CC	TIGR exons can also be used to diagnose glaucoma	
XX	SQ Sequence 5300 BP; 1483 A; 1152 C; 1234 G; 1431 T; 0 U; 0 Other;	
XX	Query Match 67.8%; Score 4067.8; DB 2; Length 5300;	
XX	Best Local Similarity 99.9%; Pred. No. 0;	
XX	Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;	

QY 1 GCTCCACAGAAAGTCTCCCACTCTAAGATTCTGCATCAAGATGTTTACAGCCAGAAAGCTC 60  
 Db 1216 GCTCCACAGAAAGTCTCCCACTCTAAGATTCTGCATCAAGATGTTTACAGCCAGAAAGCTC 1275  
 QY 61 CGTGAAGGTGAAGGTCTGTGTCTTACACTTACTGTATGCTTTACACTGAGCTCACTGC 120  
 Db 1276 CGTGAAGGTGAAGGTCTGTGTCTTACACTTACTGTATGCTTTACACTGAGCTCACTGC 1335  
 QY 121 AACCTGTGCTCCCAAGGTTCAAGCAATTCTCCGTCTGAGCTTCCCGAGTACTGGAGCT 180  
 Db 1336 AACCTGTGCTCCCAAGGTTCAAGCAATTCTCCGTCTGAGCTTCCCGAGTACTGGAGCT 1395  
 QY 181 ACAGGCGCAGCCGCGCTAATTTTGTATTTGTAGTGAAGATGGGGTTTACCATATTAG 240  
 Db 1396 ACAGGCGCAGCCGCGCTAATTTTGTATTTGTAGTGAAGATGGGGTTTACCATATTAG 1455  
 QY 241 CCGGCTGTGTTTGAATCTCTGAATCTCAAGGTATCCACCACTCAAGCTTCTTAAGTGC 300  
 Db 1456 CCGGCTGTGTTTGAATCTCTGAATCTCAAGGTATCCACCACTCAAGCTTCTTAAGTGC 1515  
 QY 301 TGGGATTAAGGATGATGATCACCGCGCCGCGCAAGGTCAGTGTATTAAATGAATTAAC 360  
 Db 1516 TGGGATTAAGGATGATGATCACCGCGCCGCGCAAGGTCAGTGTATTAAATGAATTAAC 1575  
 QY 361 TTGAATGGTTTACTAACCACAGAGGAAAACAGCAAAAGCTGTGAATTTTCAGGGATTC 420  
 Db 1576 TTGAATGGTTTACTAACCACAGAGGAAAACAGCAAAAGCTGTGAATTTTCAGGGATTC 1635  
 QY 421 TTGGGATGGGGAAATGTGTCAATGAGCTGCTGCTTACCTCCAGACCACTGTCTCTATCA 480  
 Db 1636 TTGGGATGGGGAAATGTGTCAATGAGCTGCTGCTTACCTCCAGACCACTGTCTCTATCA 1695  
 QY 481 CTTTCTCCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACCATCTTTTGTG 540  
 Db 1696 CTTTCTCCCTCATCTCATTTTTCAGGCTAAGTTACATTTTATTCACCATCTTTTGTG 1755  
 QY 541 GTAAGCTTCACATCGTTACTGAATTAAGATTAATTAATTAAGTTTGGGGCCA 600  
 Db 1756 GTAAGCTTCACATCGTTACTGAATTAAGATTAATTAATTAAGTTTGGGGCCA 1815  
 QY 601 TCTGTGTGTGTATTAAGGGAAGAGGCAATACCCAGAGACTCTTTGAAGCCCCCGGACG 660  
 Db 1816 TCTGTGTGTGTATTAAGGGAAGAGGCAATACCCAGAGACTCTTTGAAGCCCCCGGACG 1875  
 QY 661 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCAACCCGGGGTCTGGGTGCTGAGCA 720  
 Db 1876 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCAACCCGGGGTCTGGGTGCTGAGCA 1935  
 QY 721 ACCTGCGAGCCCGTGCACCTGCTGTGTTTATCACTCTTAAGGACCTGTGCTTCT 780  
 Db 1936 ACCTGCGAGCCCGTGCACCTGCTGTGTTTATCACTCTTAAGGACCTGTGCTTCT 1995  
 QY 781 AATTCTGTGTACTCGTTCAATTCATTCAGGCAATTCATTGAACAATTTATGATTAATTA 840  
 Db 1996 AATTCTGTGTACTCGTTCAATTCATTCAGGCAATTCATTGAACAATTTATGATTAATTA 2055  
 QY 841 TCTGCAGACACAGAGCAAAATGTTGACAAAGCATGACCTGACCTTCTGAGAG 900  
 Db 2056 TCTGCAGACACAGAGCAAAATGTTGACAAAGCATGACCTGACCTTCTGAGAG 2115  
 QY 901 GTGACAGTTTCTCATGGAAGAAGTGCAGAAATTAATTAAGCCAGCAATTAACCCA 960  
 Db 2116 GTGACAGTTTCTCATGGAAGAAGTGCAGAAATTAATTAAGCCAGCAATTAACCCA 2175  
 QY 961 GTGCTGAAAAGAAATTAACACATTTTGAAGATTGTGGCAGCATCTCTTAACAA 1020  
 Db 2176 GTGCTGAAAAGAAATTAACACATTTTGAAGATTGTGGCAGCATCTCTTAACAA 2235  
 QY 1021 GGCACCTCTAGAGCCCTGCTGCTCATCTGAGCCCGAGAGCCCGCAAGCCGAGT 1080  
 Db 2236 GGCACCTCTAGAGCCCTGCTGCTCATCTGAGCCCGAGAGCCCGCAAGCCGAGT 2295  
 QY 1081 CTTCAGAGCTCTCTCATCATGATCAAGCGCTGAGCTGAGCTGCTGCTTCCGCTG 1140

Db 2296 CTTCCAGCTCTCTCTCTCATCAGTCAAGGCTGACAGCTGGCTGCTCCCTTCCGCTG 2355  
 QY 1141 AATGCTCTGTGTGATCTGAGCTGAGAGCTCTTGGCTCCAGGCTCCAGAAAGAAATGG 1200  
 Db 2356 AATGCTCTGTGTGATCTGAGCTGAGAGCTCTTGGCTCCAGGCTCCAGAAAGAAATGG 2415  
 QY 1201 AGAGGAAAATCTAGTCTAACGGAATCTGAGAGGGAAGTGTTCCTCAGAGGAAAAGG 1260  
 Db 2416 AGAGGAAAATCTAGTCTAACGGAATCTGAGAGGGAAGTGTTCCTCAGAGGAAAAGG 2475  
 QY 1261 GCTTCACGTCCAGAGAAATTCAGAGAGTGGGGAATGCAAGGAGTGGGACCGTGGGAC 1320  
 Db 2476 GCTTCACGTCCAGAGAAATTCAGAGAGTGGGGAATGCAAGGAGTGGGACCGTGGGAC 2535  
 QY 1321 TGAAGGAGTGTGAAAGGACAGAAAGTGAAGAAAGGCAAGCTGAAGCTGCCAGATGTC 1380  
 Db 2536 TGAAGGAGTGTGAAAGGACAGAAAGTGAAGAAAGGCAAGCTGAAGCTGCCAGATGTC 2595  
 QY 1381 AGTGTGTTCAAGGAGCTGAGAGTGTTCCTGTGCTCTCTGTAGCTTTTATCTTTTCT 1440  
 Db 2596 AGTGTGTTCAAGGAGCTGAGAGTGTTCCTGTGCTCTCTGTAGCTTTTATCTTTTCT 2655  
 QY 1441 CTGCTTGAAGAGAAAGTCTTATGATGAAGGATGCAATTCATTAAGTCAAGCTT 1500  
 Db 2656 CTGCTTGAAGAGAAAGTCTTATGATGAAGGATGCAATTCATTAAGTCAAGCTT 2715  
 QY 1501 AAAATTCAGAGGAGTGTGATGGGTTTCTCTTCAAGAGGCTTTATTTAAATGGGAATATAG 1560  
 Db 2716 AAAATTCAGAGGAGTGTGATGGGTTTCTCTTCAAGAGGCTTTATTTAAATGGGAATATAG 2775  
 QY 1561 GAAGGAGACTATTTCTAGGCGGTAAATTCACGGAAGAAATGATGAGAGTCTTTTCT 1620  
 Db 2776 GAAGGAGACTATTTCTAGGCGGTAAATTCACGGAAGAAATGATGAGAGTCTTTTCT 2835  
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 Db 2836 CATGCTTCTGGGCACTACTCAGCTGTGTGTGAATTTGGCTTATGCAACCGTGGAA 2895  
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 Db 2896 AACCTGGAATCAGAGAGCTGAGTTTCTTCTGAGTCTGCAATGGTTGACTGTGACAC 2955  
 QY 1741 CGTGGCAAGTGTCTCTCTCTCTGAGCCATAGTCTTCTGCTATTAAGACCTTGGCA 1800  
 Db 2956 CGTGGCAAGTGTCTCTCTCTCTGAGCCATAGTCTTCTGCTATTAAGACCTTGGCA 3015  
 QY 1801 GCTCTGCTTCTGTGAACATTCCTCTGTGATTCCTGTGAGGGGGATGTTGAAGGGG 1860  
 Db 3016 GCTCTGCTTCTGTGAACATTCCTCTGTGATTCCTGTGAGGGGGATGTTGAAGGGG 3075  
 QY 1861 AAGAGGAGAGCTGAGACAGCTGAGCAAGGGAGGTGAGAGGGGACAGAGAGGACG 1920  
 Db 3076 AAGAGGAGAGCTGAGACAGCTGAGCAAGGGAGGTGAGAGGGGACAGAGAGGACG 3135  
 QY 1921 CAGAGCTGGGTGCTCATCAGTCTCTCATGATCACTGACATCCAGAGCCGAGAGCA 1980  
 Db 3136 CAGAGCTGGGTGCTCATCAGTCTCTCATGATCACTGACATCCAGAGCCGAGAGCA 3195  
 QY 1981 CAATGCTTCAGAAAAGCTCAATGAACCCACAGACCAATTTTCTTCCCTAAGCATAGAC 2040  
 Db 3196 CAATGCTTCAGAAAAGCTCAATGAACCCACAGACCAATTTTCTTCCCTAAGCATAGAC 3255  
 QY 2041 AATGCAATTCGCAATTAACCAAAAAGAAATGAGAGACTAATCTGTGTGATGCTTTGCGCTG 2100  
 Db 3256 AATGCAATTCGCAATTAACCAAAAAGAAATGAGAGACTAATCTGTGTGATGCTTTGCGCTG 3315  
 QY 2101 GCATTCAAAATCTGGGCGAGAGCAAGTGAAGAAATGCGAGATGTTTAACTTTTCAACC 2160  
 Db 3316 GCATTCAAAATCTGGGCGAGAGCAAGTGAAGAAATGCGAGATGTTTAACTTTTCAACC 3375  
 QY 2161 TGACCAAGACCCCAAGCTTCAAGATGACTGCTGACAGCAAGGATGACCTGACGCGC 2220





XX Key Location/Qualifiers  
 FT mutation 4337  
 FT /\*tag= a  
 FT /note= "Wild type C is replaced by G"  
 PN MO9832850-A1.  
 PD 30-JUL-1998.  
 PF 09-JAN-1998; 98W-US000468.  
 PR 28-JAN-1997; 97US-00791154.  
 PR 26-SEP-1997; 97US-00938669.  
 PA (R83C ) UNIV CALIFORNIA.  
 PI Nguyen TD, Polansky JR, Chen P, Chen H;  
 DR WPI, 1998-427946/36.  
 XX Use of TIGR nucleic acid sequences - used for, e.g. developing products  
 PT for diagnosis, prognosis and treatment of glaucoma.  
 PS Disclosure; Fig 2; 105p; English.  
 CC This sequence is a trabecular meshwork induced glucocorticoid response  
 CC protein (TIGR) promoter mutant, TIGRmt1, which is used in a method for  
 CC diagnosing glaucoma in a patient. The method involves the detection of  
 CC polymorphisms whose presence is predictive of a mutation affecting TIGR  
 CC response in the patient and can be diagnostic of glaucoma or steroid  
 CC sensitivity. Base substitutions and base additions upstream of and within  
 CC TIGR exons can also be used to diagnose glaucoma  
 CC  
 SQ Sequence 5300 BP; 1482 A; 1151 C; 1236 G; 1431 T; 0 U; 0 Other;  
 Query Match 67.8%; Score 4067.8; DB 2; Length 5300;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 4081; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

DB 1696 CTTTCTCCCTCATCTCATTTTCAGGCTAAGTTACATTTTATTCACCATGCTTTGTG 1755  
 QY 541 GTAAAGCTCCACATCTGTTACTGAAATAAAGCTATACATACTAAGTCCATTGGGGCCA 600  
 DB 1756 GTAAAGCTCCACATCTGTTACTGAAATAAAGCTATACATACTAAGTCCATTGGGGCCA 1815  
 QY 601 TCTGTGTGTGTATAGAGGAGAGGAGGATACCCACAGACTCCTTGAAGCCCCGGCAG 660  
 DB 1816 TCTGTGTGTGTATAGAGGAGAGGAGGATACCCACAGACTCCTTGAAGCCCCGGCAG 1875  
 QY 661 AGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCAGGGGTCTGGGTCTCTGAGCA 720  
 DB 1876 AGTTTCTCTCCAGCTGGGGAGCCCTGCAAGCACCAGGGGTCTGGGTCTCTGAGCA 1935  
 QY 721 ACCGCGACCCCGGCACTGGTTGTTTGTATACATCTCTAGGAGCTGTGCTTTCT 780  
 DB 1936 ACCGCGACCCCGGCACTGGTTGTTTGTATACATCTCTAGGAGCTGTGCTTTCT 1995  
 QY 781 ATTCTGTGTGACTGTTTCAATTCACAGGCAATTCATGACAAATTTATAGTAATTATA 840  
 DB 1996 ATTCTGTGTGACTGTTTCAATTCACAGGCAATTCATGACAAATTTATAGTAATTATA 2055  
 QY 841 TCTGCCAGACACCAAGACAAATAATGTGACAAAGCACTGCTCCTTCTGTGGAG 900  
 DB 2056 TCTGCCAGACACCAAGACAAATAATGTGACAAAGCACTGCTCCTTCTGTGGAG 2115  
 QY 901 GTGACAGTTTCTCANTGAGAGCGTGCAAGAAATTAATAGCAGCCCACTTAACCCA 960  
 DB 2116 GTGACAGTTTCTCANTGAGAGCGTGCAAGAAATTAATAGCAGCCCACTTAACCCA 2175  
 QY 961 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGCGCAGAGATCCCTTAACA 1020  
 DB 2176 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGCGCAGAGATCCCTTAACA 2235  
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 DB 2236 GGCACCTCCTTAAGGCCCTCTGCTCTCATGTGTCGCCGAGGCCCAAGCCCAAGT 2295  
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 DB 2296 CTTCCAAACCTTCCTCCATCAGTCAAGGCGTGAGCTGGCCGCTCCGCTCCCGCTG 2355  
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 DB 2356 AATGCTCTGTGTGACTGAGCTGGAGACTCCTTGACTCAGAGCTCCAGAAAGAAATAG 2415  
 QY 1201 AGAGGAAACTAGTCTAACGGAATCTGAGGGGACAGTGTCTCTCAGAGGAAAGGG 1260  
 DB 2416 AGAGGAAACTAGTCTAACGGAATCTGAGGGGACAGTGTCTCTCAGAGGAAAGGG 2475  
 QY 1261 GCTTCAAGCTCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAGTGGGAGCGTGGGGC 1320  
 DB 2476 GCTTCAAGCTCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAGTGGGAGCGTGGGGC 2535  
 QY 1321 TGAAGGGGTGTGAAGGACAGGAAGTAAAAAGGCGAAGCTGAGTCCAGATGTTTC 1380  
 DB 2536 TGAAGGGGTGTGAAGGACAGGAAGTAAAAAGGCGAAGCTGAGTCCAGATGTTTC 2595  
 QY 1381 AGTGTGTTCACGGGGCTGGGAGGTTTCCGTGCTTCTCTGAGAGCTTTTATCTTTTCT 1440  
 DB 2596 AGTGTGTTCACGGGGCTGGGAGGTTTCCGTGCTTCTCTGAGAGCTTTTATCTTTTCT 2655  
 QY 1441 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAAGGAGATGCAAGTTCAATAAGCAGTGT 1500  
 DB 2656 CTGCTTGAAGAGAAAGAGTCTAATTCATGAAAGGAGATGCAAGTTCAATAAGCAGTGT 2715  
 QY 1501 AAAAATTCAGGGGTGTGATGGGTTTCTCTTCCAGAAAGGCTTATTTAATGGAATATAG 1560  
 DB 2716 AAAAATTCAGGGGTGTGATGGGTTTCTCTTCCAGAAAGGCTTATTTAATGGAATATAG 2775  
 QY 1561 GAAGGAGTCAATTTCTAAGGCGTTAATTCAGGAAGAGTGAAGTCTTTTCTTTT 1620

Db 2776 GAAGCAGCTCATTTCTAGCCGCTTAATTCACGAAAGAAATGACGTGAGCTTTTCTTT 2835  
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Db 2836 CATGCTTTCTGGGCAACTACTACAGCCCTGTGTGGAATTGGCTTAATGCAAGCGTGAA 2895  
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Db 2896 AACCTTGGAAATCAGAGACTCGGTTTTCTTTCTGGTTCTGCAATGTTGGCTGTGCGAC 2955  
Qy 1741 CGTGGGCAAGTGTCTCTCTCCCTGGGCAATGCTTCTCTGTATTAAGACCTTTGCA 1800  
Db 2956 CGTGGGCAAGTGTCTCTCTCCCTGGGCAATGCTTCTCTGTATTAAGACCTTTGCA 3015  
Qy 1801 GCTCTGCTGTCTGTGAACACTTCCCTGTGATTTCTGTAGGGGGGATGTTGAGAGGG 1860  
Db 3016 GCTCTGCTGTCTGTGAACACTTCCCTGTGATTTCTGTAGGGGGGATGTTGAGAGGG 3075  
Qy 1861 AAGAGGCAAGCTGAGCAGCTGAGCCACAGGGGAGGTGAGGGGACAGAAAGCAGG 1920  
Db 3076 AAGAGGCAAGCTGAGCAGCTGAGCCACAGGGGAGGTGAGGGGACAGAAAGCAGG 3135  
Qy 1921 CAGAACCTGGTCTCATATAGTCTCACTGATCACTGACTCCAGACCGAGGCCA 1980  
Db 3136 CAGAACCTGGTCTCATATAGTCTCACTGATCACTGACTCCAGACCGAGGCCA 3195  
Qy 1981 CAATGCTTCAAGAAAGCTCAATGACCCAAACAGCCCAATTTTCTTCCCTAAGCATAGAC 2040  
Db 3196 CAATGCTTCAAGAAAGCTCAATGACCCAAACAGCCCAATTTTCTTCCCTAAGCATAGAC 3255  
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Db 3256 AATGCAATTTGGCCAAATTAACAAAAGAAATGACAGACATACCTGGTGTAGCTTTTGGCT 3315  
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Qy 2161 TGAACGACACCCCAACGAGCTCAGCAGTGACTGTACAGCAGCAGAGTGAACCTGACGCG 2220  
Db 3376 TGAACGACACCCCAACGAGCTCAGCAGTGACTGTACAGCAGCAGAGTGAACCTGACGCG 3435  
Qy 2221 AAGGAGGAGAAAGAAAGAAAGAGAGTGTATGACAAAGAAAGACAGATTCATTCAG 2280  
Db 3436 AAGGAGGAGAAAGAAAGAAAGAGAGTGTATGACAAAGAAAGACAGATTCATTCAG 3495  
Qy 2281 GGCAGTGTGGAATTTGACCAAGGATTAATGTCACGTGATCTGGGTTCTAGAGGCAAG 2340  
Db 3496 GGCAGTGTGGAATTTGACCAAGGATTAATGTCACGTGATCTGGGTTCTAGAGGCAAG 3555  
Qy 2341 GCTATATTGGGGGGGAAAAAATCACTGCAAGGGAAGTGGGAGACCTGATTTTCTAATAC 2400  
Db 3556 GCTATATTGGGGGGGAAAAAATCACTGCAAGGGAAGTGGGAGACCTGATTTTCTAATAC 3615  
Qy 2401 TATATTTTCTTTTCAAGCTGATTAATCTGAGCAAGTCAACAAGGTAGTAACTGAGGCT 2460  
Db 3616 TATATTTTCTTTTCAAGCTGATTAATCTGAGCAAGTCAACAAGGTAGTAACTGAGGCT 3675  
Qy 2461 GTAAGATTACTAATGTTCTCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA 2520  
Db 3676 GTAAGATTACTAATGTTCTCTCTTATTAAGAACTCTTTTCTCTGTGAGTTAGCAGACA 3735  
Qy 2521 AAGGCAATCCCGTTTCTTTTAAACAGAGAAAGAAACCTTCTAAGAGTAAAGCCAAACAGAT 2580  
Db 3736 AAGGCAATCCCGTTTCTTTTAAACAGAGAAAGAAACCTTCTAAGAGTAAAGCCAAACAGAT 3795  
Qy 2581 TCAAGCTAAGTCTTGCTGACTATATGATGTGTTTTTTTGAAGAAATCAATTCAGCGATGT 2640  
Db 3796 TCAAGCTAAGTCTTGCTGACTATATGATGTGTTTTTTTGAAGAAATCAATTCAGCGATGT 3855  
Qy 2641 TACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAAACACCAT 2700  
Db 3856 TACTATCTGATTCAGAAATGAGACTAGTACCCTTTGGTCACTGTAAACAAACACCAT 3915

Qy 2701 TTGTAATGCTCAAGTTGAGGCTTAACAGCAAGCAATCAAAATAGAAATGATCTTT 2760  
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Qy 2881 ATTAATTCAGGGGCTTAAGTTACTCTGACAGCTTTGGTATTAATTAATGCTATGGC 2940  
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Qy 2941 ATTTGCTTTTGTCTTCTTGTGGGTTTATTAATGTAAGCAGGGAATTAATTAACCTAC 3000  
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Qy 3001 AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTAATTTTGTTTTACACCTT 3060  
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Qy 3061 CTAACTAAATTTAACAATTTTATTCATTCAGGAAATGAGCATTAACCTCAAGGTGTAAT 3120  
Db 4276 CTAACTAAATTTAACAATTTTATTCATTCAGGAAATGAGCATTAACCTCAAGGTGTAAT 4335  
Qy 3121 ACAGTACCTGTGATTTGTCACTTAACAAATAGAAATCAAGACATTTTACTATATTACA 3180  
Db 4336 ACAGTACCTGTGATTTGTCACTTAACAAATAGAAATCAAGACATTTTACTATATTACA 4395  
Qy 3181 GTTGTGCAATAGCTGTGAATGTAATTTTAACTCAAAACATACTTTGAATTAAGACC 3240  
Db 4396 GTTGTGCAATAGCTGTGAATGTAATTTTAACTCAAAACATACTTTGAATTAAGACC 4455  
Qy 3241 TCCGCTGGATCTGTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3300  
Db 4456 TCCGCTGGATCTGTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4515  
Qy 3301 TATCATATTTCAATATCAATTTGTTCTTGTGTAATTAATTAATTAATTAATTAATTA 3360  
Db 4516 TATCATATTTCAATATCAATTTGTTCTTGTGTAATTAATTAATTAATTAATTAATTA 4575  
Qy 3361 TCTTTCTGAGAAAGTCCCAAGATTTTCAACAATGAGGTTCTTGGCATGCAACACAG 3420  
Db 4576 TCTTTCTGAGAAAGTCCCAAGATTTTCAACAATGAGGTTCTTGGCATGCAACACAG 4635  
Qy 3421 AGTAAGAACTGATTTTGAAGGCTTAACATTTGACATTTGCTGAGATGCAAGCTGAATT 3480  
Db 4636 AGTAAGAACTGATTTTGAAGGCTTAACATTTGACATTTGCTGAGATGCAAGCTGAATT 4695  
Qy 3481 AGAAAGTCTCCCAAGAAATACAGTGTGTTTAAAGTAAAGGAGTGAAGGGGAAAAATGCG 3540  
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Qy 3541 CGCTTCTAATAGAAATGCTCTCCCTGAGCCTGTAAGGAGTGTCTTGTGTCTGAGCTG 3600  
Db 4756 CGCTTCTAATAGAAATGCTCTCCCTGAGCCTGTAAGGAGTGTCTTGTGTCTGAGCTG 4815  
Qy 3601 GCTGTATTTTCTCTGTGCTCTGCTGCTGCTTAAGAGACTGTGTAATCTCCAGATTCCT 3660  
Db 4816 GCTGTATTTTCTCTGTGCTCTGCTGCTGCTTAAGAGACTGTGTAATCTCCAGATTCCT 4875  
Qy 3661 AGCATAGTCCCTGAGCAGTCAAGTCTCAATGAGTTTGAAGAGTGAATGGAATATATA 3720  
Db 4876 AGCATAGTCCCTGAGCAGTCAAGTCTCAATGAGTTTGAAGAGTGAATGGAATATATA 4935  
Qy 3721 ACTGAAGATATATCTTGTGAAATCAGACACCAAGTATGCTGTGATGATGTGTATAC 3780  
Db 4936 ACTGAAGATATATCTTGTGAAATCAGACACCAAGTATGCTGTGATGATGTGTATAC 4995









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Db 1276 CGTAGAGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTAGCTCACTGC 1335
QY 121 AACCTGTGCTCCAGAGTTCAAGCAATTTCTCTGTCTCAGCCTCCGCGTAAAGCTGGAGCT 180
Db 1336 AACCTGTGCTCCAGAGTTCAAGCAATTTCTCTGTCTCAGCCTCCGCGTAAAGCTGGAGCT 1395
QY 181 ACAGGCGCACGCGCGCTAAATTTTGTATTTAGTATGAGATGGGGTTTCAACATATATAG 240
Db 1396 ACAGGCGCACGCGCGCTAAATTTTGTATTTAGTATGAGATGGGGTTTCAACATATATAG 1455
QY 241 CCGCGTGTGTTTGAATCTCTGACCTCAGGTATCCACCACTCAGCTCTCTAAAGTGC 300
Db 1456 CCGCGTGTGTTTGAATCTCTGACCTCAGGTATCCACCACTCAGCTCTCTAAAGTGC 1515
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Db 1516 TGGGATTAACAGCATGATGACCGCGCCGCGCAAGGGTCAAGTTTAATTAAGAAATAC 1575
QY 361 TTGAATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTATTAATTTCAAGGATTC 420
Db 1576 TTGAATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTATTAATTTCAAGGATTC 1635
QY 421 TTGGGATGGGGAAATGGTCCATGAGCTGCTGCTTATGTCACAGCACTGGTCTTCATCA 480
Db 1636 TTGGGATGGGGAAATGGTCCATGAGCTGCTGCTTATGTCACAGCACTGGTCTTCATCA 1695
QY 481 CTTTCTTCCCTCATCTCTCATTTTCAGGCTAAGTTACATTTTATTCACATGCTTTTGTG 540
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QY 541 GTAAAGCTTCACATCGTTACTGAAATAGATATACATAAATAGTTTCAATTTGGGGCA 600
Db 1756 GTAAAGCTTCACATCGTTACTGAAATAGATATACATAAATAGTTTCAATTTGGGGCA 1815
QY 601 TCTGTGTGTGTATATAGGGAGAGAGGGCAATCCCAAGACCTCTTGAAGCCCGGCGAG 660
Db 1816 TCTGTGTGTGTATATAGGGAGAGAGGGCAATCCCAAGACCTCTTGAAGCCCGGCGAG 1875
QY 661 AAGTTTCTCTCAGCTGGGGGAGCCCTGCAGACACCGGGGCTCGGGTGTCTGAGAG 720
Db 1876 AAGTTTCTCTCAGCTGGGGGAGCCCTGCAGACACCGGGGCTCGGGTGTCTGAGAG 1935
QY 721 AACTGCAGCCCGGTGCACCTGGTGTGTTTGTATCACTCTCTAGGAGCTGTGTCTTCT 780
Db 1936 AACTGCAGCCCGGTGCACCTGGTGTGTTTGTATCACTCTCTAGGAGCTGTGTCTTCT 1995
QY 781 AATTTCTGTGTACTGTTCATTCATTCAGGCAATTCATTGACAAATTTATGAGTACTTATA 840
Db 1996 AATTTCTGTGTACTGTTCATTCATTCAGGCAATTCATTGACAAATTTATGAGTACTTATA 2055
QY 841 TCTGCAGACACCAAGAGCAAAATGTGTAGCAAAAGCATGCTGCCCTTCTGTGAG 900
Db 2056 TCTGCAGACACCAAGAGCAAAATGTGTAGCAAAAGCATGCTGCCCTTCTGTGAG 2115
QY 901 GTGACAGTTTCTCATGTAAGAGGTGCAAGAAATTAATAGCCAGCCAACTTAAACCA 960
Db 2116 GTGACAGTTTCTCATGTAAGAGGTGCAAGAAATTAATAGCCAGCCAACTTAAACCA 2175
QY 961 GTGCTGAAGAAAGAAATTAACACCATTTGAAAGATTTGCGGAGCATTCCTTAACA 1020
Db 2176 GTGCTGAAGAAAGAAATTAACACCATTTGAAAGATTTGCGGAGCATTCCTTAACA 2235
QY 1021 GGGCACTTCCCTAGGGGCCCCGCTGCTCCATTCGTCCTCCGAGGCCCCCAAGCCCGAGT 1080
Db 2236 GGGCACTTCCCTAGGGGCCCCGCTGCTCCATTCGTCCTCCGAGGCCCCCAAGCCCGAGT 2295
QY 1081 CTTTCAAGCTTCTCTCATGATCAAGCTGCAAGCTGAGCTGAGCTCTGCTTCCCGT 1140
Db 2286 CTTTCAAGCTTCTCTCATGATCAAGCTGCAAGCTGAGCTGAGCTCTGCTTCCCGT 2355
QY 1141 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGGCTTCAGGCTTCAGAAAGAAATAG 1200
Db 2356 AATGCTCTGTGTGATCTGAGCTGAGACTCTTGGCTTCAGGCTTCAGAAAGAAATAG 2415
QY 1201 AAGAGGAACCTAGTCTTAAGGGAATCTGAGAGGGAACATGTTTCTTCAAGAGAAAGG 1260
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QY 1261 GCCTCCAGCTCCAGAGGAATTCACAGAGGTGGGAGCTGCAAGGAGTGGGGAACGCTGGGG 1320
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QY 1321 TGAAGCGGTGTGAAAGGCAAGGTGAAAGGCAAGGCTGAAGCTGCCAGATGTTTC 1380
Db 2536 TGAAGCGGTGTGAAAGGCAAGGTGAAAGGCAAGGCTGAAGCTGCCAGATGTTTC 2595
QY 1381 AGTGTGTTTCAAGGGGCTGGGAGTTTCCGTTGCTTCCGTGAGCTTTTATCTTTTCT 1440
Db 2596 AGTGTGTTTCAAGGGGCTGGGAGTTTCCGTTGCTTCCGTGAGCTTTTATCTTTTCT 2655
QY 1441 CTGCTTGAAGAGAAAGTCTAATTCATGAAGGATGACGTTTCAATAAGTCAAGCTGTT 1500
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QY 1501 AAAATTCAGAGGTGTGATGGTGTTCCTTCAAGAGGCTTTATTTAATGGGAATATAG 1560
Db 2716 AAAATTCAGAGGTGTGATGGTGTTCCTTCAAGAGGCTTTAATTTAATGGGAATATAG 2775
QY 1561 GAAAGGAGCTATTTCTTACGCGCTTAAATTCACGAAAGATGACTGAGTCTTTTCTTT 1620
Db 2776 GAAAGGAGCTATTTCTTACGCGCTTAAATTCACGAAAGATGACTGAGTCTTTTCTTT 2835
QY 1621 CATGCTTCTGGGCAACTACTAGCCCTGTGTGAGCTTGGCTTATGCAAGCGGTGCA 1680
Db 2836 CATGCTTCTGGGCAACTACTAGCCCTGTGTGAGCTTGGCTTATGCAAGCGGTGCA 2895
QY 1681 AACCTTGAATCAGAGACTGGGTTTCTTCTGTGTTCTGCAATGTTGGCTGTGCGAC 1740
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QY 1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGTATTAAGCCCTTGCA 1800
Db 2956 CGTGGGCAAGTGTCTCTCTTCCCTGGGCAATAGTCTTCTGTATTAAGCCCTTGCA 3015
QY 1801 GCTCTGATCTGTGGAACATTCCTCTGTGATTCCTGTGAGGGGGATGTTGAAGGGG 1860
Db 3016 GCTCTGATCTGTGGAACATTCCTCTGTGATTCCTGTGAGGGGGATGTTGAAGGGG 3075
QY 1861 AAGAGGCAAGCTGAGCAGCTGAGCCACAGGGAGGTGAGGGGGAACAGAAAGCAGG 1920
Db 3076 AAGAGGCAAGCTGAGCAGCTGAGCCACAGGGAGGTGAGGGGGAACAGAAAGCAGG 3135
QY 1921 CAGAACTGGGTGCTCCATCAGTCTCTCATGTATCACTGATCACTGACATCCAGAACGCA 1980
Db 3136 CAGAACTGGGTGCTCCATCAGTCTCTCATGTATCACTGATCACTGACATCCAGAACGCA 3195
QY 1981 CAATGCTTCAGAGAAAGCTCAATGAACCCACAGCAACATTTTCTTCCCTTAAGCTAAG 2040
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QY 2221 AGGGAGAGAGAAAGAAAGAGAGGGAATGATATGAGCAAGAAAGACATTCATTCAG 2280
Db 3436 AGGGAGAGAGAAAGAAAGAGAGGGAATGATATGAGCAAGAAAGACATTCATTCAG 3495
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Oy	2281	GGCAGTGGGAAATTGACCA	CAGGGAGTTTATGACCA	CGGATCTCGGGTTC	CTAAGGACGAGG	2340
Db	3496	GGCAGTGGGAAATTGACCA	CAGGGAGTTTATGACCA	CGGATCTCGGGTTC	CTAAGGAGGACGAG	3555
Oy	2341	GCTATATTTGTTGGGGGGG	AAAAATCAGTTC	CAAGGAGTCCGGAGAC	CTGTATTTCTATATAC	2400
Db	3556	GCTATATTTGTTGGGGGGG	AAAAATCAGTTC	CAAGGAGTCCGGAGAC	CTGTATTTCTATATAC	3615
Oy	2401	TATATTTTTCCTTTTAC	AAGCTGAGTAAATTC	TGAGCAAGTCA	CAAGGTATGTAATCTGAGGCT	2460
Db	3616	TATATTTTTCCTTTTAC	AAGCTGAGTAAATTC	TGAGCAAGTCA	CAAGGTATGTAATCTGAGGCT	3675
Oy	2461	GTAAGATTACTAGTTCCT	CTTATTTAGAACTCTTTT	CTCTGTGAGTTAGAC	GACACA	2520
Db	3676	GTAAGATTACTAGTTCCT	CTTATTTAGAACTCTTTT	CTCTGTGAGTTAGAC	GACACA	3735
Oy	2521	AGGGCAATCCCGTTTCT	TTTAAACAGAGAA	GAACATTCCTA	AGTAAGCCAAACAGAT	2580
Db	3726	AGGGCAATCCCGTTTCT	TTTAAACAGAGAA	GAACATTCCTA	AGTAAGCCAAACAGAT	3795
Oy	2581	TCAAGCCCTAAGTCTTG	CTGACTATATATGTTGG	TTTTTGGAAAAATCA	TTTACAGGATGT	2640
Db	3796	TCAAGCCCTAAGTCTTG	CTGACTATATATGTTGG	TTTTTGGAAAAATCA	TTTACAGGATGT	3855
Oy	2641	TACTATCTGATTCAGAA	AAATGAGACTAGACCT	TTGGTGCAGCTGTAA	CAAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAA	AAATGAGACTAGACCT	TTGGTGCAGCTGTAA	CAAAACCCAT	3915
Oy	2701	TTGTATATGTCTCAAG	TTCAGGCTTAACTG	CAAGCAACCAATCA	TAATTAAGATAGATCTTT	2760
Db	3916	TTGTATATGTCTCAAG	TTCAGGCTTAACTG	CAAGCAACCAATCA	TAATTAAGATAGATCTTT	3975
Oy	2761	AGAGCAAACTGTGTCT	CCACTCGAGAGTGAGT	CTCCACGAGGCACTGT	GGAAATATTT	2820
Db	3976	AGAGCAAACTGTGTCT	CCACTCGAGAGTGAGT	CTCCACGAGGCACTGT	GGAAATATTT	4035
Oy	2821	ACTTCAACAATTTGAC	ACCTGTGTGGTATTTA	CAACATTAAGTTGCT	CAAGGCAATC	2880
Db	4036	ACTTCAACAATTTGAC	ACCTGTGTGGTATTTA	CAACATTAAGTTGCT	CAAGGCAATC	4095
Oy	2881	ATTATTTCAAGTGGCT	TTAAGTAACTTCGAC	AGTTTGGATATTTA	TGGCATAATGGC	2940
Db	4096	ATTATTTCAAGTGGCT	TTAAGTAACTTCGAC	AGTTTGGATATTTA	TGGCATAATGGC	4155
Oy	2941	ATTTCCTTTTGTTTTCT	CTCTTGGGTTTATAT	GTAAAGCAGGATTTA	TAACTACCTAC	3000
Db	4156	ATTTCCTTTTGTTTTCT	CTCTTGGGTTTATAT	GTAAAGCAGGATTTA	TAACTACCTAC	4215
Oy	3001	AGTCCAGAAAGCCTGT	GAAATTTGAATGAG	AAAAAATTACATTTT	TGTTTAAACACCTT	3060
Db	4216	AGTCCAGAAAGCCTGT	GAAATTTGAATGAG	AAAAAATTACATTTT	TGTTTAAACACCTT	4275
Oy	3061	CTAACTAAATTTAAC	ATTTTATTCATTTG	CGCAATGAGCCAT	TAACCTCAAAAGTGTATATA	3120
Db	4276	CTAACTAAATTTAAC	ATTTTATTCATTTG	CGCAATGAGCCAT	TAACCTCAAAAGTGTATATA	4335
Oy	3121	ACAAGTACCTGTGAT	TTTGTCAATTACCA	ATAGAAATCAGAC	CATTTTATTAATCTATATTTACA	3180
Db	4336	ACAAGTACCTGTGAT	TTTGTCAATTACCA	ATAGAAATCAGAC	CATTTTATTAATCTATATTTACA	4395
Oy	3181	GTGTGTTGCGAATAC	GTGTGTAAGTGAATAT	TTTATCTCAAAA	CTATCTTTTGGAAATTTAAC	3240
Db	4396	GTGTGTTGCGAATAC	GTGTGTAAGTGAATAT	TTTATCTCAAAA	CTATCTTTTGGAAATTTAAC	4455
Oy	3241	TCTCTGTGATCTTGT	TTTTTAAACATTTA	ATTAACATGTTTAA	AAATTTTATATATTTTGA	3300
Db	4456	TCTCTGTGATCTTGT	TTTTTAAACATTTA	ATTAACATGTTTAA	AAATTTTATATATTTTGA	4515
Oy	3301	TATATCATATTTCA	TATATCATTTGTTTCT	TTTGTATCTATATTTT	TATATATTTGAAAAACA	3360
Db	4516	TATATCATATTTCA	TATATCATTTGTTTCT	TTTGTATCTATATTTT	TATATATTTGAAAAACA	4575

OY	3361	TCCTTTCGAGAAAGAGTCCCCAGATTCACCAATGAGGCTCTGGCATGCAACACAG	3320
Db	4576	TCCTTCGAGAAAGAGTCCCCAGATTCACCAATGAGGCTCTGGCATGCAACACAG	4635
OY	3421	AGTAAAGACTGATTTAAGGCTAACTTGAATTGTGCTGAGATGCAAGCTGAATT	3480
Db	4636	AGTAAAGACTGATTTAAGGCTAACTTGAATTGTGCTGAGATGCAAGCTGAATT	4695
OY	3481	AGAAAGTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTGAGGGGGAAATCTGC	3540
Db	4696	AGAAAGTCTCCCAAGATACACAGTTGTTTAAAGCTAGGGGTGAGGGGGAAATCTGC	4755
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Db	4756	CGCTTCATAGAAATGCTCTCCCGAGAGCCGTGAGGGGTGCTGCTGTGTTCTGGCTG	4815
OY	3601	GCTGTATATTTTCTCTGCTCCCTGTACGTCCTTAAAGACTGTTTGGATCTCCAGTCTC	3660
Db	4816	GCTGTATATTTTCTCTGCTCCCTGTACGTCCTTAAAGACTGTTTGGATCTCCAGTCTC	4875
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Db	4876	AGCATAGTGCCTGGACAGTGCAGGTTCTCAATGAGTTTGACAGTGAATGAAATATTA	4935
OY	3721	ACTAGAAATATATCTCTGTGAAATTCAGCACACAGTAAAGCTCGATGATGATGCTAC	3780
Db	4936	ACTAGAAATATATCTCTGTGAAATTCAGCACACAGTAAAGCTCGATGATGATGCTAC	4995
OY	3781	-----GTGTGTGTGTGTGTGTGTGTGTGTAAACAGGTGAGATATAGAACTATT	3834
Db	4996	GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAACAGGTGAGATATAGAACTATT	5055
OY	3835	ATTGGGGTATGGGTGCATAAATTGGATGTTCTTTTAAAGAACTCCAAACAGCTT	3894
Db	5056	ATTGGGGTATGGGTGCATAAATTGGATGTTCTTTTAAAGAACTCCAAACAGCTT	5115
OY	3895	CTGGAAGGTTATTTTCTAAAGATCTGTCTGGACGTGGAAGGCAAACCCCTGTGCAG	3954
Db	5116	CTGGAAGGTTATTTTCTAAAGATCTGTCTGGACGTGGAAGGCAAACCCCTGTGCAG	5175
OY	3955	CCCCACCAAGCTCAAGTGCACACTGTCTTCCCCCATGAAGAGCTGCTCCCACTA	4014
Db	5176	CCCCACCAAGCTCAAGTGCACACTGTCTTCCCCCATGAAGAGCTGCTCCCACTA	5235
OY	4015	TATATAAACCTCTCTGAGCTCAGGCATGAGCCAGCAAGGCCACCCATCCAGCACTCT	4074
Db	5236	TATATAAACCTCTCTGAGCTCAGGCATGAGCCAGCAAGGCCACCCATCCAGCACTCT	5295
OY	4075	CAGCACAGC 4083	
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Search completed: March 24, 2006, 02:09:10  
Job time : 3214 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 01:29:42 ; Search time 20443 Seconds  
(without alignments)  
13731.962 Million cell updates/sec

Title: SEQ1-4037A  
Perfect score: 6000  
Sequence: 1 gctccacaggaagctctcccc.....atacgaggagctattgtac 6000

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664.4	11.1	756	3	B1821411 603038284
2	654	10.9	654	3	CA391750 ca18e04.y
3	653.8	10.9	877	6	CD172504 AGENCOURT
4	628.2	10.5	937	7	B1818249 603032468
5	611.8	10.2	635	6	CA392464 cs25b03.y
6	607	10.1	607	7	CV574677 ce27d04.y
7	604	10.1	1515	10	AY416721 Homo sapi
8	598.4	10.0	608	3	BP382502 BP382502
9	590.4	9.8	622	6	CD607955 56053818H
10	583	9.7	583	3	BP343359 BP343359
11	582.4	9.7	584	3	BP341455 BP341455
12	581.2	9.7	617	6	CD607956 56053818U
13	581	9.7	581	3	BP260344 BP260344
14	581	9.7	581	3	BP342027 BP342027
15	580.4	9.7	582	3	BP341905 BP341905
16	578.4	9.6	580	3	BP342858 BP342858
17	577.4	9.6	579	7	CV030235 9283 Full
18	560.6	9.3	567	3	BP368724 BP368724
19	531	8.8	531	6	CA395551 cs65h08.y
20	525.6	8.8	540	1	AU298286 AU298286
21	512.6	8.5	1497	10	AY416722 Pan trogl
22	501.4	8.4	503	6	CA395272 cs62d03.y

23	498.4	8.3	500	6	CA394815 cs66g05.y
24	469	7.8	469	2	BP725009 bx1a12.y
25	464.6	7.7	472	3	BP342996 BP342996
26	461	7.7	478	1	AU297866 AU297866
27	459	7.6	460	5	BK483934 DKF2p6861
28	433.6	7.2	466	5	BY733575 BY733575
29	429	7.1	429	2	BF726094 bx23h10.y
30	417.8	7.0	611	7	CK625411 m13g12.y
31	412.8	6.9	633	8	DN425956 LIB4216-0
32	409.4	6.8	1515	10	AY416723 Mus muscu
33	404.8	6.7	601	7	CK624800 m125d05.y
34	404.4	6.7	598	7	CK625171 m129h12.y
35	393.8	6.6	398	6	CA394076 cs46h09.y
36	384.4	6.4	582	2	BP365528 BP365528
37	383.8	6.4	404	6	CD677941 ho24f06.y
38	378.8	6.3	966	6	CD515039 AGENCOURT
39	371	6.2	371	6	CA391298 cs13e03.y
40	343.8	5.7	627	1	BB024293 BB024293
41	340.8	5.7	539	3	BI540290 45313 MA
42	317.2	5.3	601	2	BB617903 BB617903
43	297.6	5.0	604	1	AU298485 AU298485
44	278.4	4.6	568	3	BP259864 BP259864
45	234.6	3.9	345	5	BY337559 BY337559

## ALIGNMENTS

RESULT 1  
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DEFINITION mRNA sequence.  
B1821411  
ACCESSION B1821411.1 GI:15932961  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniota; Vertebrate; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 756)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: csapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: LAM11446 row: h column: 21  
High quality sequence stop: 754.  
Location/Qualifiers  
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/clone\_id="NIH\_MGC\_115"  
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male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (BcoRI site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruher (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH\_MGC Library."

Query Match 11.1%; Score 664.4; DB 3; Length 756;  
 Best Local Similarity 99.8%; Pred. No. 4.5e-106;  
 Matches 665; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

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 1 CATCCAGGACCTCTCAGACAGACAGAGCTTTCCAGAGAGAGCTTCCAGAGAGCTTCTGCA 60

4120 ATGAGGTTCTTCTGTGACAGGTTCTGACAGCTTTGGGCTTGAGATGCCAGCTGTCCAGCTG 4179  
 61 ATGAGGTTCTTCTGTGACAGGTTCTGACAGCTTTGGGCTTGAGATGCCAGCTGTCCAGCTG 120

4180 CTGCTTCTGGCCCTGCTGTGAGGAGTGTGGGGGCGAGAGAGCTAGCTCAGAGAGGCGC 4239  
 121 CTGCTTCTGGCCCTGCTGTGAGGAGTGTGGGGGCGAGAGAGCTAGCTCAGAGAGGCGC 180

4240 AATGACCAAGATGGCCGATGCCAGTATACCTTCACTGATGAGCCAGTCCCAATGATCAGC 4299  
 181 AATGACCAAGATGGCCGATGCCAGTATACCTTCACTGATGAGCCAGTCCCAATGATCAGC 240

4300 TGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4359  
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4360 CAACGCTTGAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4419  
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4420 CAATTGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4479  
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4540 GCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4599  
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4600 CAGAAGAAATGAGATCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4659  
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4660 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4719  
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4720 GAAGGT 4725  
 661 GAAGGT 666

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 LOCUS CA391750  
 DEFINITION c818e04.y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone c818e04  
 5', mRNA sequence.

ACCESSION CA391750.1 GI:24723905  
 VERSION CA391750  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 BUKAYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 654)  
 Wiatow,G., Bernstein,S.L., Wyatt,M.K., Parfitt,R.N., Behal,A.,  
 Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

TITLE  
 JOURNAL  
 PUMED  
 COMMENT

Expressed sequence tag analysis of human RPE/choroid for the  
 NEIRank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 Mol. Vis. 8 (4), 205-220 (2002)  
 12107410  
 Contact: Wiatow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/311, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graham@helix.nih.gov  
 Plate: 18 row: e column: 04  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

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 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
 eyes (75-80 years old) yielded approximately 600 mg of  
 dissected RPE/choroid tissue. This in turn yielded 340 ug  
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
 library in the pCMVSPORT6 vector was constructed at Life  
 Technologies (Rockville, MD; now part of Invitrogen Corp),  
 essentially following the protocols of the Superscript  
 Plasmid System (Invitrogen Corp).  
 <http://www.invitrogen.com/>). The library code  
 designation was cs. For this library, cDNA inserts were  
 cloned into the NotI/Mlu sites of the vector. EST  
 analysis was performed on the unamplified library at the  
 NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 10.9%; Score 654; DB 6; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-104;  
 Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 ACCCATCCAGGACCTCTCAGACAGACAGAGCTTTCCAGAGAGAGCTTCCAGAGAGCTTCT 60

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4177 CTGCTGCTTCTGGCCCTGCTGTGAGGAGTGTGGGGGCGAGAGAGCTAGCTCAGAGAGAG 4236  
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4237 GCCAATGACCAAGATGGCCGATGCCAGTATACCTTCACTGATGAGCCAGTCCCAATGATCC 4296  
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4297 AGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4356  
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4417 CACCAATGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4476  
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Db 481 ACTGCTTACAGCAACCTCTCCGAGACAGTCAAGTTCTGAGAGAAAGAAAGGACTA 540  
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ACCESSION CD172504  
VERSION CD172504.1 GI:30854135  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 877)  
NIH-MGC http://mhc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM437 row: e column: 08  
High quality sequence stop: 739.  
Location/Qualifiers

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insert size 1.42 kb. Library was constructed by  
(Invitrogen). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 10.9%; Score 653.8; DB 6; Length 877;  
Best Local Similarity 99.7%; Pred.No.3.2e-104;  
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Db 61 TTCTGTGACGTTGTCTGACGCTTTGGGCTGAGATGCCAGCTGTCCAGCTGCTTCTG 120

Qy 4189 GCTTCCCTGTGTGGATGTGTGGGGCCAGACAGCTCAGTCCAGAAAGCCCAATGACCG 4248  
Db 121 GCTTCCCTGTGTGGATGTGTGGGGCCAGACAGCTCAGTCCAGAAAGCCCAATGACCG 180  
Qy 4249 AGTGGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAAATCAGCTGCCAGAG 4308  
Db 181 AGTGGCCGATGCCAGTATACCTTCAGTGTGGCCAGTCCCAATGAAATCAGCTGCCAGAG 240  
Qy 4309 CAGAGCCGAGCCATGTCAATCATCATTAATTACAGAGAGCAGAGAGCCCAAGCTTA 4368  
Db 241 CAGAGCCGAGCCATGTCAATCATCATTAATTACAGAGAGCAGAGAGCCCAAGCTTA 300  
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Db 361 TTGACACAGGCTGCCAGGCCCCAGAGAGCCAGAGAGGGGCTGCAGAGGAGCTGGGACCC 420  
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Qy 4609 GAGATCTGGCCAGAGAGTTGGAAGCAGCAGCCAGAGAGGTAGCAGAGCTGAGAGGGGC 4668  
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Qy 4669 CAGTGTCCCGAGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGT 4725  
Db 601 CAGTGTCCCGAGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGAGAAAGT 657

RESULT 4  
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LOCUS B03032468P1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5173673 5',  
DEFINITION mRNA sequence.  
ACCESSION B1818249  
VERSION B1818249.1 GI:15928689  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 937)  
NIH-MGC http://mhc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1432 row: g column: 18  
High quality sequence stop: 839.  
Location/Qualifiers

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DB 301 CTCCTCCACCAATTGACCTTGGACGAGCTGCCAGGCCCCCAGAGAGACCCAGAGAGGGGCTG 360
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DB 361 CAGAGGAGCTGGGCACTCTGAGGCGGGAAGCGGAGACCACTGGAAACCCAAACCAAGAG 420
QY 4531 TTGGAGACTGCTTACGACCAACCTCTCCGAGCAAGTCACTTCTGGAGGAAGAAGAAG 4590
DB 421 TTGGAGACTGCTTACGACCAACCTCTCCGAGCAAGTCACTTCTGGAGGAAGAAGAAG 480
QY 4591 CGACTAAGGCAAGAAATGAGATCTGACCAAGGTTGGAAGCAGCCAGAGAGTA 4650
DB 481 CGACTAAGGCAAGAAATGAGATCTGACCAAGGTTGGAAGCAGCCAGAGAGTA 540
QY 4651 GCAGAGCTGAGAGAGGGGCAAGTGTCCCGAGACCCGAGACACTGCTCGGGCTGTGCCACCA 4710
DB 541 GCAGAGCTGAGAGAGGGGCAAGTGTCCCGAGACCCGAGACACTGCTCGGGCTGTGCCACCA 600
QY 4711 GGCTCCAGAGAGGT 4725
DB 601 GGCTCCAGAGAGGT 615

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RESULT 6
CV574677 607 bp mRNA linear EST 22-OCT-2004
LOCUS 0e27d04.y1 Human keratocornus cornea, unamplified, (od/oe) Homo
ACCESSION CV574677
VERSION CV574677.1 GI:54479490
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarhontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 607)
Rabinowitz,Y., Dong,L. and Wistow,G.
Expressed sequence tag analysis of human keratocornus cornea
Unpublished (2004)
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 27 row: d column: 04
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..607
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="0e27d04"
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/dev_stage="Adult"
/lab_host="EMD10B"
/clone_lib="Human keratocornus cornea, unamplified,
(od/oe)"

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note="Organ: Eye; Vector: pCMVSPORT6; Approximately 40ug total RNA was extracted from 7 adult human keratocornus corneas. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com). First strand synthesis was carried out using a Not I primer-adaptor [5'-TGACTAGTTCTAGATCCGAGCGGCCGCTT)15-3']. cDNA was cloned in Not I/Sal I sites. Est analysis was performed on

the unamplified library at the NIH Intramural Sequencing Center (NISC)."

Query Match 10.1%; Score 607; DB 7; Length 607;  
Best Local Similarity 100.0%; Pred. No. 5.4e-96;  
Matches 607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4073 CTCACACAGAGAGCTTTCCAGAGAAAGCTCCACCAAGCTCTGCAATGAGTCTTCT 4132
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QY 4133 GTGACGTTGTCAGCTTTTGAGGCTGAGATCCAGCTGTCAGTGTGCTTCTGAGCT 4192
DB 61 GTGACGTTGTCAGCTTTTGAGGCTGAGATCCAGCTGTCAGTGTGCTTCTGAGCT 120
QY 4193 GCTTGTTGGATGTGGGGGCGAGACAGCTCAGCTCAGAGAGCCAAATGCAAGTGTG 4252
DB 121 GCTTGTTGGATGTGGGGGCGAGACAGCTCAGCTCAGAGAGCCAAATGCAAGTGTG 180
QY 4253 GCCATGTCATATTAACCTTCACTGCTGAGTCCCAATGAATCCAGCTGCCAGACGA 4312
DB 181 GCCATGTCATATTAACCTTCACTGCTGAGTCCCAATGAATCCAGCTGCCAGACGA 240
QY 4313 GCCAGGCCATGTCATATTAACCTTCACTGAGTCCCAATGAATCCAGCTGCCAGACGA 4372
DB 241 GCCAGGCCATGTCATATTAACCTTCACTGAGTCCCAATGAATCCAGCTGCCAGACGA 300
QY 4373 TGGAGGCCCAAAAGCTGACTCAGCTCCCTGAGAGAGCTCCTCCCAATTTGACCTTGG 4432
DB 301 TGGAGGCCCAAAAGCTGACTCAGCTCCCTGAGAGAGCTCCTCCCAATTTGACCTTGG 360
QY 4433 ACCAGGCTGTCAGAGCCCCCAGAGAGACCCAGAGAGGCTGCAAGAGAGTGGGACCTTGA 4492
DB 361 ACCAGGCTGTCAGAGCCCCCAGAGAGACCCAGAGAGGCTGCAAGAGAGTGGGACCTTGA 420
QY 4493 GGCGGAGCGGAGACAGCTGGAACCCAAACCAAGAGTGTGAGACTGCTTACAGCAACC 4552
DB 421 GGCGGAGCGGAGACAGCTGGAACCCAAACCAAGAGTGTGAGACTGCTTACAGCAACC 480
QY 4553 TCCTCCGAGACAGTCAAGTTCTGAGAGAGAGAGAGCGACTAAGGCAGAAATGAGA 4612
DB 481 TCCTCCGAGACAGTCAAGTTCTGAGAGAGAGAGAGCGACTAAGGCAGAAATGAGA 540
QY 4613 ATCTGGCCAGAGAGTTGGAAGACAGCCAGAGAGTGAAGGCTGAGAGAGGGCCAGT 4672
DB 541 ATCTGGCCAGAGAGTTGGAAGACAGCCAGAGAGTGAAGGCTGAGAGAGGGCCAGT 600
QY 4673 GTCCCA 4679
DB 601 GTCCCA 607

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RESULT 7
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AY116721 genomic survey sequence.
ACCESSION AY116721
VERSION AY116721.1 GI:39772681
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarhontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1515)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

```

TITLE

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1515)  
AUTHORS Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,  
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.C.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submissions  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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source  
1..1515  
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Best Local Similarity 100.0%; Pred.No.1.6e-95;  
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4120 ATGAGGTTCTTCTGTGCAAGTTGCTGAGCTTGGGCTTGATGCAAGTCTCCAGCTG 4179  
DB 1 ATAGAGTTCTTCTGTGCAAGTTGCTGAGCTTGGGCTTGATGCAAGTCTCCAGCTG 60  
QY 4180 CTGCTTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4239  
DB 61 CTGCTTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 4240 AATGACCAAGTGGCCGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4299  
DB 121 AATGACCAAGTGGCCGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 4300 TGCCCAAGACAGAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4359  
DB 181 TGCCCAAGACAGAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
QY 4360 CAAAGCTTTAGACCTGGAAGGCTCAAAAGCTGCACTGAGCTCCCTGGAAGCTCTTCCAC 4419  
DB 241 CAAAGCTTTAGACCTGGAAGGCTCAAAAGCTGCACTGAGCTCCCTGGAAGCTCTTCCAC 300  
QY 4420 CAAATTGACCTTTGACCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTG 4479  
DB 301 CAAATTGACCTTTGACCAAGGCTGCTGCAAGGCTGCTGCAAGGCTGCTGCAAGGCTG 360  
QY 4480 CTGGGCACTCTGAGAGCGGAGCGGAGCCAGCTGGAACCCAAACCAAGAGTTGAGACT 4539  
DB 361 CTGGGCACTCTGAGAGCGGAGCGGAGCCAGCTGGAACCCAAACCAAGAGTTGAGACT 420  
QY 4540 GCTTACAGCAACTCTCTCCAGACCAAGTCAAGTTCTGAGGAGAGAGAAAGCACTAAG 4599  
DB 421 GCTTACAGCAACTCTCTCCAGACCAAGTCAAGTTCTGAGGAGAGAGAAAGCACTAAG 480  
QY 4600 CAAAGAAAATGAGATCTGGGCAAGAGTTGGAAGCAAGCAAGCAAGAGGTTAGAAAGCTG 4659  
DB 481 CAAAGAAAATGAGATCTGGGCAAGAGTTGGAAGCAAGCAAGCAAGAGGTTAGAAAGCTG 540  
QY 4660 AGAAGGGGCGAGTGTCCCGAGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGA 4719  
DB 541 AGAAGGGGCGAGTGTCCCGAGACCCGAGACACTGCTGGGCTGTGCCACAGGCTCCAGA 600  
QY 4720 GAAG 4723  
DB 601 GAAG 604  
RESULT 8  
BP382502

LOCUS BP382502 608 bp mRNA linear EST 21-SEP-2004  
DEFINITION BP382502 Sugano cDNA library, adipose tissue Homo sapiens cDNA  
clone adSH02027, mRNA sequence.  
ACCESSION BP382502  
VERSION BP382502.1 GI:52418461  
KEYWORDS EST.  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 608)  
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,  
Mizushima-Sugano,J., Nakai,K. and Sugano,S.  
Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
Genome Res. 14 (9), 1711-1718 (2004)  
JOURNAL 15342556  
PUBMED  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
FEATURES  
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Query Match 10.0%; Score 598.4; DB 3; Length 608;  
Best Local Similarity 99.0%; Pred.No.1.7e-94;  
Matches 602; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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DB 1 TATTTTCTAAGATCTTGTGTCAGCTGTAAGGCAACCCCTGTGCAAGGCCCAACCA 60  
QY 3964 GCTCAGCTGGCCACTCTGTCTTCTCCCATTAAGGCTGGTCCCAATATATTAAC 4023  
DB 61 GCTCAGCTGGCCACTCTGTCTTCTCCCATTAAGGCTGGTCCCAATATATTAAC 120  
QY 4024 CTCTGAGAGCTCAGGCATGAGCCAGCAAGGCCAATCCATCCAGGACCTCTGAGACAGC 4083  
DB 121 CTCTGAGAGCTCAGGCATGAGCCAGCAAGGCCAATCCATCCAGGACCTCTGAGACAGC 180  
QY 4084 AGAGCTTTTCAGAGGAAGCTTCAAGGCTTGTCAATGAGGTTCTTGTGCAAGTTGC 4143  
DB 181 AGAGCTTTTCAGAGGAAGCTTCAAGGCTTGTCAATGAGGTTCTTGTGCAAGTTGC 240  
QY 4144 TGCAAGTTTGGGCTGAGATGTCACAGTGTCCAGCTGTCTTCTGAGGCTGAGTGG 4203  
DB 241 TGCAAGTTTGGGCTGAGATGTCACAGTGTCCAGCTGTCTTCTGAGGCTGAGTGG 300  
QY 4204 GATGTGGGGCCAGGACAGCTCAGCTCAGAGAAAGCCCAATGACCAAGTGGCCGATGCCAG 4263  
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QY 4264 TATACCTTCAAGTGTGGCCAGTCCCAATGAATCAAGTGTCCAGAGCAAGCCAGGCTATG 4323  
DB 361 TATACCTTCAAGTGTGGCCAGTCCCAATGAATCAAGTGTCCAGAGCAAGCCAGGCTATG 420  
QY 4324 TCAGTATCATTAATCTTAAGAGAGACAGACAGCAACCAAGCTTGAAGGCTGAGGCTAC 4383  
DB 421 TCAGTATCATTAATCTTAAGAGAGACAGACAGCAACCAAGCTTGAAGGCTGAGGCTAC 480  
QY 4384 AAAGCTGACCTAGCTCCCTGGAGAGCTCTCCACCAATTGACCTTGAACCAAGGCTGCC 4443  
DB 481 AAAGCTGACCTAGCTCCCTGGAGAGCTCTCCACCAATTGACCTTGAACCAAGGCTGCC 540

4444 AGCCCCAGAGACCAGAGGGGCTGCAGAGGAGCTGGGAGCCCTTGAGGGCGGAGCGG 4503  
DB 541 AGCCCCAGAGACCAGAGGGGCTGCAGAGGAGGAGCTGGGAGCCCTTGAGGGCGGAGCGG 600  
QY 4504 GACCCAGCT 4511  
DB 601 GACCCAGCT 608

RESULT 9  
LOCUS CD607955 622 bp mRNA linear EST 12-JAN-2004  
DEFINITION 56053818H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD607955  
VERSION CD607955.1 GI:40256218  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo  
REFERENCE 1 (bases 1 to 622)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
JOURNAL Genomics 84 (1), 205-210 (2004)  
PUBMED 15203218  
COMMENT Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers

FEATURES  
Source 1..622  
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Best Local Similarity 97.9%; Pred. No. 4.4e-93;  
Matches 609; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

QY 4062 TCACGACCTCTCTGACACAGACAGGCTTTCCAGAGAGAGCTCCCAAGCTCTGCAT 4121  
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QY 4122 GAGGTTCTCTGTCGACCTTCTGACGTTTGGGCTTGAAGTGCAGCTCTCCAGCTGCT 4181  
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QY 4182 GCTTCTGACCTGCTGATGTGGGATGTGGGAGCCAGACAGCTCAGTCAAGAGGCCAA 4241  
DB 121 GCTTCTGACCTGCTGATGTGGGATGTGGGAGCCAGACAGCTCAGTCAAGAGGCCAA 180  
QY 4242 TGACCAAGTGGCCGATGACGATATACCTTCAAGTGTGACAGTCCCAATGATCCAGCTG 4301  
DB 181 TGACCAAGTGGCCGATGACGATATACCTTCAAGTGTGACAGTCCCAATGATCCAGCTG 240  
QY 4302 CCCAGAGAGAGCCAGGACGATGTCAGTATCACTTAATTACAGAGAGACAGACAGCCCA 4361  
DB 241 CCCAGAGAGAGCCAGGACGATGTCAGTATCACTTAATTACAGAGAGACAGACAGCCCA 300  
QY 4362 AGCTTAGACCTGAGGACCAAAAGCTGAGTCACTGCTCCCTGAGAGAGCTCTTCCACCA 4421  
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QY 4422 ATTGACCTTGAACCAAGGCTGCAGGCTCCAGAGAGCCAGAGAGAGGAGGCTGCAAGGAGCT 4481  
DB 361 ATTGACCTTGAACCAAGGCTGCAGGCTCCAGAGAGCCAGAGAGAGGAGGCTGCAAGGAGCT 420

QY 4482 GGGACCTCTGAGGCGGAGCGGAGCCAGCTGGAACCCAAACCAAGAGATTGAGAGATGC 4541  
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QY 4542 CTACAGCAACTCTCTCCGAGACAAATGATCTTGTGAGAGAGAGAGAGAGCACTTAAGCA 4601  
DB 481 CTACAGCAACTCTCTCCGAGACAAATGATCTTGTGAGAGAGAGAGAGAGCACTTAAGCA 540  
QY 4602 AG--AAATGGAATTCTGCGCCAGAGAGTTGGAAGACGACCCAGAGAGTGCAGAGCTG 4659  
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QY 4660 AGAAGGCGCCAGTGTCCCAAGA 4681  
DB 601 AGAAGGCGCCAGTGTCCCAAGA 622

RESULT 10  
LOCUS BP343359 583 bp mRNA linear EST 17-SEP-2004  
DEFINITION BP343359 Sugano cDNA library, stomach mucosa Homo sapiens cDNA  
ACCESSION BP343359  
VERSION BP343359.1 GI:52273246  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo  
REFERENCE 1 (bases 1 to 583)  
AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,  
Mizushima-Sugano, J., Nakai, K. and Sugano, S.  
TITLE Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
PUBMED 15342556  
COMMENT Contact: Yureka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yezukhi@ims.u-tokyo.ac.jp.  
Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 8.8e-92;  
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4048 AGCAAGGCCAACCCATCCAGGACCTCTGACACAGACAGCTTTCCAGAGAGAGCTTCAC 4107  
DB 1 AGCAAGGCCAACCCATCCAGGACCTCTGACACAGACAGCTTTCCAGAGAGAGCTTCAC 60  
QY 4108 CAAGCTCTGCAATGAGATTCTTCTGTGCAAGTGTGCTGCAAGCTTTGGGCTCTGAGATGCCA 4167  
DB 61 CAAGCTCTGCAATGAGATTCTTCTGTGCAAGTGTGCTGCAAGCTTTGGGCTCTGAGATGCCA 120  
QY 4168 GCTGTCCAGCTGCTGCTTCTGCGCTGCTGTGTGAGATGTGGGAGCCAGAGAGCTCAG 4227  
DB 121 GCTGTCCAGCTGCTGCTTCTGCGCTGCTGTGTGAGATGTGGGAGCCAGAGAGCTCAG 180  
QY 4228 CTACAGAAAGCCAAATGACCAAGAGTGGCCGATGCCAGTATACCTTCACTGTGGCAGTCCC 4287  
DB 181 CTACAGAAAGCCAAATGACCAAGAGTGGCCGATGCCAGTATACCTTCACTGTGGCAGTCCC 240  
QY 4288 AATGAATTCAGCTGCCAGAGACCAAGGCCATGTCACTATCCATTAACAGAGA 4347



Db 241 AATGAATCCAGTGCCTCCAGAGAGAGCCAGGCCATGTCAATCATTAATTAACAGAGA 300  
 Oy 4348 GACAGAGAGACCCAAAGCTTTAAGACCTGAGAGCCACCAAGCTGACTGCTGAG 4407  
 Db 301 GACAGAGAGACCCAAAGCTTTAAGACCTGAGAGCCACCAAGCTGACTGCTGAG 360  
 Oy 4408 AGCCTCTCCACCAATTGAACCTTGAACAGGCTGCCAGGCCCAAGAGAGAGAG 4467  
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 Oy 4468 CTGCAAGAGAGAGCTGGGCAACCTGAGAGCCGAGAGACCACTGGAACCCAAACCA 4527  
 Db 421 CTGCAAGAGAGAGCTGGGCAACCTGAGAGCCGAGAGACCACTGGAACCCAAACCA 480  
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 Db 481 GAGTTGAGAGCTGCTTACAGCAACCTCTCTCCAGACCAAGTCAGTTCTGAGAGAGAG 540  
 Oy 4588 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGG 4630  
 Db 541 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGG 583

RESULT 11  
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 LOCUS BP341455 Sugano cDNA library, stomach mucosa Homo sapiens cDNA  
 DEFINITION clone STM02509, mRNA sequence.  
 ACCESSION BP341455  
 VERSION BP341455.1 GI:52271175  
 KEYWORDS EST.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens (human)  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 584)  
 Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,  
 Mizushima-Sugano J., Nakai K. and Sugano S.  
 Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 Genome Res. 14 (9), 1711-1718 (2004)  
 15342556  
 JOURNAL  
 PUBMED  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ime.u-tokyo.ac.jp.  
 Location/Qualifiers  
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Query Match 9.7%; Score 582.4; DB 3; Length 584;  
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 Oy 4108 CAAGCTCTGCATGAGGTTCTTCTGTGACGTTGTGACGCTTGGGCTTGAGATGCCA 4167  
 Db 61 CAAGCTCTGCATGAGGTTCTTCTGTGACGTTGTGACGCTTGGGCTTGAGATGCCA 120  
 Oy 4168 GCTGTCAAGTGTGCTTCTGTGAGCTGTGCTGTGAGATGTGGGGCCAGAGAGCTCAG 4227

Db 121 GCTGTCCAGCTGCTCTTCTGAGCTGCTGCTGTGGATGTGGGGCCAGAGAGCTCAG 180  
 Oy 4228 CTCAAGAAAGCCCAATGACCAAGATGGCCGATGCCAGTATTAATCTTCACTGTGCCAGTCCC 4287  
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 Oy 4288 AATGAATCCAGTGTCCCAAGAGACAGAGCCAGGCCATGTATCATTAATTAACAGAGA 4347  
 Db 241 AATGAATCCAGTGTCCCAAGAGACAGAGCCAGGCCATGTATCATTAATTAACAGAGA 300  
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 Db 541 AAGCGACTAAGCGCAAGAAATGAAATCTGGCCAGAGAGTTGGA 584

RESULT 12  
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 DEFINITION CD607956  
 ACCESSION CD607956.1 GI:40256219  
 VERSION CD607956.1 GI:40256219  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 617)  
 Fu G.K., Wang J.T., Yang J., Au-Young J. and Stuve J.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 15203218  
 JOURNAL  
 PUBMED  
 CONTACT: FU GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.  
 Location/Qualifiers  
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FEATURES  
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 Location/Qualifiers

## ORIGIN

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Qy 4182 GCTTCGGCTGCTGCTGTTGGGATGTTGGGGGCGCAGGACAGTTCACTTCAGGAAGGCCAA 4241  
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Db 198 GGGACACCTTGAGGCGGAGCGGAGCCAGCTGAGAAACCCAAACAGAGAGTTGAGAGCTGC 139  
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Db 18 AAGGTG 13

RESULT 13  
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LOCUS BP260344 Sugano cDNA library, heart Homo sapiens cDNA clone  
DEFINITION HRT09556, mRNA sequence.  
ACCESSION BP260344  
VERSION BP260344.1 GI:52175575  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Suzuki.Y., Yamashita.R., Shiota.M., Sakakibara.Y., Chiba.J.,  
Mizushima-Sugano.J., Nakai.K. and Sugano.S.  
TITLE Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
PUBMED 15342556  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
Location/Qualifiers  
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Db 421 AGGGGCTGCAAGGAGAGCTGCGACCTGAGGCGGAGAGCGGAGCAAGCTGAGAAACCCAA 480  
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DEFINITION BP342027  
ACCESSION BP342027  
VERSION BP342027.1 GI:52271793  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 581)  
AUTHORS Suzuki.Y., Yamashita.R., Shiota.M., Sakakibara.Y., Chiba.J.,  
Mizushima-Sugano.J., Nakai.K. and Sugano.S.  
TITLE Sequence comparison of human and mouse genes reveals a homologous  
block structure in the promoter regions  
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
PUBMED 15342556  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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Best Local Similarity 100.0%;  Pred. NC 2e-91;
Matches 581;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0

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	Clone SIM03586, mRNA sequence.

ACCESSION	BP341905
VERSION	BP341905.1
KEYWORDS	GI:52271664
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	1 (bases 1 to 582)
AUTHORS	Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

**TITLE**  
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions  
**JOURNAL**  
Genome Res. 14 (9), 1711-1718 (2004)  
**PUBMED**  
15342556

COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES Location/Qualifiers  
1..582

SOURCE

Department of Virology

Institute of Medical Science, University of Tokyo  
4-6-1 Shirokane, Minato-ku, Tokyo 108-8538, Japan

Email: yevgeny.k@nrc.gov

Location/Qualifiers

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U.S. DEPARTMENT OF AGRICULTURE

ORIGIN

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QY	4283	GTCCCAATGAATCCAGCTGTCCAGAGCAGAGCCAGGCCATGTCACTCATCTAACTTAC	4343
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QY	4343	AGAGAGACAGACACCCCAAGCTTAACTGTGAGGCCACCAAGACTGACTCACTCCC	4403
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QY	4403	TGGAGAGCTCTCCACCAATTGAACCTTGGACCAAGCTGTGCCAGGCCCCAGAGACCCAG	4463
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Job time : 20448 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table:  
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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7	4015.8	66.9	5271	3	US-09-306-828-34
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9	2773.4	46.2	2800	3	US-10-017-870-10
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43	189.8	3.2	29326	3	US-09-949-016-15356	Sequence 15356, A
44	184.6	3.1	205044	3	US-09-949-016-15851	Sequence 15851, A
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## ALIGNMENTS

RESULT 1  
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; Patent No. 6171788  
; GENERAL INFORMATION:  
; APPLICANT: Nguyen, Thai D.  
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
; TITLE OF INVENTION: RELATED DISEASES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Howrey & Simon  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,669A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/791,154  
; FILING DATE: 28-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mendelson, Elliot  
; REGISTRATION NUMBER: P-42,878  
; REFERENCE/DOCKET NUMBER: 07425-0034  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 383-6857  
; TELEFAX: 202 383-6610  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6169 base pairs  
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; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-938-669A-3  
Query Match 81.5%; Score 4888.8; DB 3; Length 6169;

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QY 1381 AGTGTGTTCAAGGAGCTGGAGTGTTCCTGTTGCTTCTGTGAGCCTTTTATCTTTCT 1440
Db 2596 AGTGTGTTCAAGGAGCTGGAGTGTTCCTGTTGCTTCTGTGAGCCTTTTATCTTTCT 2655
QY 1441 CTGCTTGAAGAGAAAGATCTAATTCATGAAGGAGATGCAATTAAGTCAAGCTGTT 1500
Db 2656 CTGCTTGAAGAGAAAGATCTAATTCATGAAGGAGATGCAATTAAGTCAAGCTGTT 2715
QY 1501 AAAATTCAGGAGTGTGCAATGGGTTTCTTTCACAGAGGCTTTAATTAATGGAATATAG 1560
Db 2716 AAAATTCAGGAGTGTGCAATGGGTTTCTTTCACAGAGGCTTTAATTAATGGAATATAG 2775
QY 1561 GAAAGAGCTCAATTCCTAGGCGGTTAATTCACGGAAGAAATGACTGGAGTCTTTCTTT 1620
Db 2776 GAAAGAGCTCAATTCCTAGGCGGTTAATTCACGGAAGAAATGACTGGAGTCTTTCTTT 2835
QY 1621 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGTGACTTGTGCTTATGCAAGACGCTGCA 1680
Db 2836 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGTGACTTGTGCTTATGCAAGACGCTGCA 2895
QY 1681 AACTTGGAAATCAGAGACTGGTTTTCTTTCTGGTTCTGTCATTTGTTGCTGTGAC 1740
Db 2896 AACTTGGAAATCAGAGACTGGTTTTCTTTCTGGTTCTGTCATTTGTTGCTGTGAC 2955
QY 1741 CGTGGCAAGTGTCTCTCTTCCCTGGGCAATGCTTCTCTGTATTAAGACCTTGCA 1800
Db 2956 CGTGGCAAGTGTCTCTCTTCCCTGGGCAATGCTTCTCTGTATTAAGACCTTGCA 3015
QY 1801 GCTCTCGTGTCTGTGAACAATTCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGGG 1860
Db 3016 GCTCTCGTGTCTGTGAACAATTCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGGG 3075
QY 1861 AAGAGGACAGAGCTGAGACCTGAGCCACAGGGAGGTGAGAGGGGACAGAGGCAAG 1920
Db 3076 AAGAGGACAGAGCTGAGACCTGAGCCACAGGGAGGTGAGAGGGGACAGAGGCAAG 3135
QY 1921 CAGAGGCTGGGTCTCCATCATGCTCTCATGATCAATCCATCAAGGACCGGAGGCA 1980
Db 3136 CAGAGGCTGGGTCTCCATCATGCTCTCATGATCAATCCATCAAGGACCGGAGGCA 3195
QY 1981 CAATGCTTCAGGAAAGCTCAATGAACCAAGACCAATTTTCTTCCCTAAGCATAGAC 2040
Db 3196 CAATGCTTCAGGAAAGCTCAATGAACCAAGACCAATTTTCTTCCCTAAGCATAGAC 3255
QY 2041 AATGGCAATTTGCCAATAACAAAGAAATGACAGACTTAATCTGTGTGAGCTTTTGCTG 2100
Db 3256 AATGGCAATTTGCCAATAACAAAGAAATGACAGACTTAATCTGTGTGAGCTTTTGCTG 3315
QY 2101 GCATTCAAAAATCTGGGCGAGAGCAAGTGGAAATATGCGAGAAATTTTAACTTTTACACC 2160
Db 3316 GCATTCAAAAATCTGGGCGAGAGCAAGTGGAAATATGCGAGAAATTTTAACTTTTACACC 3375

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QY	2161	THACCAAGCACCCACAGCAGCTCAGACGTGACTGCTGACACGACCGAGCTGCAGCGC	2220
Db	3376	THACCAGACACCCACAGCAGCTCAGCAGTGACTGCTGACACGACCGAGTGACTGCAGCGC	3435
QY	2221	AGGGAGGAGGAAGAAAAAGAGGGGATAGTGTATGAGCAAGAAAGACAGATTCACTTCAG	2280
Db	3436	AGGGAGGAGGAAGAAAAAGAGGGGATAGTGTATGAGCAAGAAAGACAGATTCACTTCAG	3495
QY	2281	GGCAGTGGGAATTGACCAACAGGAATTATAGTCAACGTGACTCTGGTCTAGAGGCAGG	2340
Db	3496	GGCAGTGGGAATTGACCAACAGGAATTATAGTCACTGATCTGGGTTCTAGAGGCAGG	3555
QY	2341	GCTATTTCGTGGGGGGGAAAAATTCAGTTCAAGGAAAGTCGGGACCTGATTTCTATAC	2400
Db	3556	GCTATTTCGTGGGGGGGAAAAATTCAGTTCAAGGAAAGTCGGGACCTGATTTCTATAC	3615
QY	2401	TATATTTTTCTTTTCAAGCTGAGTAATTTGAGCAATCAACAGGTGTAACAGGCT	2460
Db	3616	TATATTTTTCTTTTCAAGCTGAGTAATTTGAGCAATCAACAGGTGTAACAGGCT	3675
QY	2461	GTAAGATTACTTAAGTTTCTCCTTATTAAGAACTCTTTTCTCTGAGTTAGACACACA	2520
Db	3676	GTAAGATTACTTAAGTTTCTCCTTATTAAGAACTCTTTTCTCTGAGTTAGACACACA	3735
QY	2521	AGGGCAATCCCGTTCTTTTAAACAGAAAGAAAACCTCTPAAGGTAAAGCAACAGAT	2580
Db	3736	AGGGCAATCCCGTTCTTTTAAACAGAAAGAAAACCTCTPAAGGTAAAGCAACAGAT	3795
QY	2581	TCAGCCTAAGCTCTTGCTGACTATATGATGGTTTTTGA AAAATCATTTCAAGCATGTT	2640
Db	3796	TCAGCCTAAGCTCTTGCTGACTATATGATGGTTTTTGA AAAATCATTTCAAGCATGTT	3855
QY	2641	TACTATCTGATTACAAAAATGAGACTACTACCCCTTGGTCAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTACAAAAATGAGACTACTACCCCTTGGTCAGCTGTAAACAAACCCAG	3915
QY	2701	TTGTAAATGTCTCAGATTCAAGGCTTAACTGACAGAACCAATCAAAATTAAGATAGATCTTT	2760
Db	3916	TTGTAAATGTCTCAGATTCAAGGCTTAACTGACAGAACCAATCAAAATTAAGATCTTT	3974
QY	2761	AGAGCAAACTGTGTTCTCCAC-TCGAGAGTGAGTGCACAGGCAAGTTGAAATATT	2819
Db	3975	AGAGCAAACTGTGTTCTCCACATCTGAGGTGAGTGCACAGGCAAGTTGAAATATT	4034
QY	2820	TACTTCACAAGATTTGACACTGTTGGTGTATTAACAACATAAAGTGTCTCAAGGCAAT	2879
Db	4035	TACTTCACAAGATTTGACACTGTTGGTGTATTAACAACATAAAGTGTCTCAAGGCAAT	4094
QY	2880	CATTATTTCAAGTGGCTTAAAGTTACTCTGACAGTTTTGGTATATTAATTTGGCTATTGC	2939
Db	4095	CATTATTTCAAGTGGCTTAAAGTTACTCTGACAGTTTTGGTATATTAATTTGGCTATTGC	4154
QY	2940	CATTTCCTTTTGGTTTTTCTCTTGGGTTATTAATGTAAAGACGGATTAATTAACCTTA	2999
Db	4155	CATTTCCTTTTGGTTTTTCTCTTGGGTTATTAATGTAAAGACGGATTAATTAACCTTA	4214
QY	3000	CAGTCCAGAAAGCCTGTGATTTGAATGACGAAAAAATTAATCAATTTGTTTTTACCACT	3059
Db	4215	CAGTCCAGAAAGCCTGTGATTTGAATGACGAAAAAATTAATCAATTTGTTTTTACCACT	4274
QY	3060	TCTTAACCTAAATTTAAACATTTTATTCCTGATGCGAATAGAGCCATTAACCTCAAGTGTAAAT	3119
Db	4275	TCTTAACCTAAATTTAAACATTTTATTCCTGATGCGAATAGAGCCATTAACCTCAAGTGTAAAT	4334
QY	3120	AACAGTACTGTGATTTTGTCAATACCAATGGAATCAACAGATTTTATATCTATATTAAC	3179
Db	4335	AACAGTACTGTGATTTTGTCAATACCAATGGAATCAACAGATTTTATATCTATATTAAC	4394
QY	3180	AGTTGTTGAGATACGTTTGAAGTAATTTTATCTCAAAACTACTTTGAAATTAAGAC	3239
Db	4395	AGTTGTTGAGATACGTTTGAAGTAATTTTATCTCAAAACTACTTTGAAATTAAGAC	4454

[illegible]

Db	5535	GCACATGTCATCTCAATTAACTTTACAGAGAGACAGACCCAAACCTTAAAGCTTGGAG	5594
Qy	4378	GCACACCAAAAGCTCGACTCAAGCTCCCTGAGAGCCTCTTCCACCAATTGACCTTGGACAG	4437
Db	5595	GCCACCAAAAGCTCGACTCAGCTCCCTGAGAGCCTCTTCCACCAATTGACCTTGGACAG	5654
Qy	4438	GCTGCACAGGCCCCCAGAGAGACCCACAGAGGGGGCTGACAGAGGAGAGCTGGGCAACCTTGAAGCGG	4497
Db	5655	GCTGCACAGGCCCCCAGAGAGACCCACAGAGGGGGCTGACAGAGGAGAGCTTGGGCAACCTTGAAGCGG	5714
Qy	4498	GAGCGGGACCAAGCTGGAAACCCAAACACAGAGAGTTGAGAGCTGGCTACAGCAACCTTCTC	4557
Db	5715	GAGCGGGACCAAGCTGGAAACCCAAACACAGAGAGTTGAGAGCTGGCTACAGCAACCTTCTC	5774
Qy	4558	CGAACAACAAGTAGTTCCTGAGAGAAAGAGAGAGGAGCTAAAGGCCAAGAAATATGAAATCTG	4617
Db	5775	CGAACAACAAGTAGTTCCTGAGAGAAAGAGAGAGGAGCTAAAGGCCAAGAAATATGAAATCTG	5834
Qy	4618	GCCAGAGAGTTGGAAAGCAGCAGCCAGAGAGGTAGCAAGGCTGAGAAAGGGGCACTGTCTCC	4677
Db	5835	GCCAGAGAGTTGGAAAGCAGCAGCCAGAGAGGTAGCAAGGCTGAGAAAGGGGCACTGTCTCC	5894
Qy	4678	CAGAACCCGAGACACTGCTCCGGGGCTGTGCACACAGGCTCCAGAGAAAGTTAAGAAATGACAGAG	4737
Db	5895	CAGAACCCGAGACACTGCTCCGGGGCTGTGCACACAGGCTCCAGAGAAAGTTAAGAAATGACAGAG	5954
Qy	4738	TGGGGGGGACTCTGAGTTTCAGCAGGTGATATGGCTCGTAGTGAACCTGTACAGGGCGCTCCA	4797
Db	5955	TGGGGGGGACTCTGAGTTTCAGCAGGTGATATGGCTCGTAGTGAACCTGTACAGGGCGCTCCA	6014
Qy	4798	GGCTTCCTCCCTGGCTGGCTTTTCTCTTAGAGATCTGCACAGCTATGACACAAAGACAGATGAATTA	4857
Db	6015	GGCTTCCTCCCTGGCTGGCTTTTCTCTTAGAGATCTGCACAGCTATGACACAAAGACAGATGAATTA	6070
Qy	4858	AGGAAGACACAGCGATCACTTCAAGTTTACTAGTAAATTAGTCTCCGAGAGCTTCATT	4917
Db	6071	AGGAAGACACACGATCACTTCAAGTTTACTAGTAAATTAGTCTCCGAGAGCTTCATT	6129
Qy	4918	TAGATTAGTGTTCAGAGTTCTGTGGCCCTTCATGTCAG	4957
Db	6130	TAGATTAGTGTTCAGAGTTCTGTGGCCCTTCATGTCAG	6169

RESULT 2  
US-09-306-828-3  
; Sequence 3, Application US/09306828

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: GENERAL INFORMATION:
: APPLICANT: Nguyen, Thai D.
: APPLICANT: Polansky, Jon R.
: APPLICANT: Chen, Pu
: APPLICANT: Chen, Hua
: TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
: CURRENT APPLICATION NUMBER: US/09/306,828
: CURRENT FILING DATE: 1999-05-07
: EARLIER APPLICATION NUMBER: US 09/227,881
: EARLIER FILING DATE: 1999-01-11
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft word 97
: SEQ ID NO 3
: LENGTH: 6169
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-306-828-3

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Query Match	81.5%	Score 4888.8;	DB 3;	Length 6169;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 4949; Conservative	0;	Mismatches 2;	Indels 9;	Gaps

QY 1 GCTCCACAGGAAGTCTCCCCACTTAGACTTTCGATCATCAGATGTTCAGCCAGAGCTC 60

Db 1216 GCTCCACAGGAAGTCTCCCCACTTAGACTTTCGATCATCAGATGTTCAGCCAGAGCTC 1275

QY	61	CGTAGAGGTAGAGGTCTGTGTCTTTACACCTACCTGTATGTCTACACCTGAGCTCACTGC	120
Db	1276	CGTAGAGGTAGAGGTCTGTGTCTTTACACCTACCTGTATGTCTACACCTGAGCTCACTGC	1335
QY	121	AACCTGTGCTCCCAAGGTTCAAGCAATTCTCTGTCTCAGCCTCCCGCGTAGTGGGACT	180
Db	1336	AACCTGTGCTCCCAAGGTTCAAGCAATTCTCTGTCTCAGCCTCCCGCGTAGTGGGACT	1395
QY	181	ACAGCGCGACGCCCGGCTAATTTTGTATTTGTATAGTATAGATAGGGGTTTACCATATTTAG	240
Db	1396	ACAGCGCGACGCCCGGCTAATTTTGTATTTGTATAGTATAGATAGGGGTTTACCATATTTAG	1455
QY	241	CCCGGCTGTCTTTAACTCTGACCTCAGAGTGAATCCACCACTCAGCCTCCTAAAGTGC	300
Db	1456	CCCGGCTGTCTTTAACTCTGACCTCAGAGTGAATCCACCACTCAGCCTCCTAAAGTGC	1515
QY	301	TGGGATTAACAGGACATGAGTCAACCGCGCCCGCCCAAGGGTCAAGTGTATTAATAGAAATAC	360
Db	1516	TGGGATTAACAGGACATGAGTCAACCGCGCCCGCCCAAGGGTCAAGTGTATTAATAGAAATAC	1575
QY	361	TTGAATGGTTTACTTAACCAACAGGGGAAACAGACAAAGCTGTGATATTTTCAGGGATTTC	420
Db	1576	TTGAATGGTTTACTTAACCAACAGGGGAAACAGACAAAGCTGTGATATTTTCAGGGATTTC	1635
QY	421	TTGGGATGGGAAATGATGCCATGATGCTGCTGCTAGTCCAGACCACTGATCTCATCA	480
Db	1636	TTGGGATGGGAAATGATGCCATGATGCTGCTGCTAGTCCAGACCACTGATCTCATCA	1695
QY	481	CTTTCTTCCTCATCTCCATCTTTTCAGGCTAGTATGCATTTTATTTACACATGCTTTTGTG	540
Db	1696	CTTTCTTCCTCATCTCCATCTTTTCAGGCTAGTATGCATTTTATTTACACATGCTTTTGTG	1755
QY	541	GTAAGCCTCCACATCTGTTACTGAATATAGATATACATTAAGTATTCATTTTGAGGCCA	600
Db	1756	GTAAGCCTCCACATCTGTTACTGAATATAGATATACATTAAGTATTCATTTTGAGGCCA	1815
QY	601	TCTGTGTGTGTATATAGGGAGAGAGGGCATCCCAAGACTCCTTGAAGCCCCCGGAC	660
Db	1816	TCTGTGTGTGTATATAGGGAGAGAGGGCATCCCAAGACTCCTTGAAGCCCCCGGAC	1875
QY	661	AGGTTTCCTCCACGCTGGGGGAAACCTGTGACAGACCCCGGGGTCTGGGTGTCCTGACGA	720
Db	1876	AGGTTTCCTCCACGCTGGGGGAAACCTGTGACAGACCCCGGGGTCTGGGTGTCCTGACGA	1935
QY	721	ACCTGCCAGCCCGTGCACCTGATGTTGTTTATCACTCTCTAGAGGACTGTGTCCTTCT	780
Db	1936	ACCTGCCAGCCCGTGCACCTGATGTTGTTTATCACTCTCTAGAGGACTGTGTCCTTCT	1995
QY	781	ATTTCGTGTGACCTCGTTCAATTCAATCCAGGATTCATTCAGCAATTTATTTAGTACTATATA	840
Db	1996	ATTTCGTGTGACCTCGTTCAATTCAATCCAGGATTCATTCAGCAATTTATTTAGTACTATATA	2055
QY	841	TCTGCACAGACACAGAGACAATAATGATGACAAAGCAGTCACTGCCCTACCTTCGTGAG	900
Db	2056	TCTGCACAGACACAGAGACAATAATGATGACAAAGCAGTCACTGCCCTACCTTCGTGAG	2115
QY	901	GTGACAGTTTCTCATGAGAAAGCTGACAGAGAAATTAATGACCGCCAACTTTAAACCA	960
Db	2116	GTGACAGTTTCTCATGAGAAAGCTGACAGAGAAATTAATGACCGCCAACTTTAAACCA	2175
QY	961	GTGCTGAAGAAAGGAATTAACACCATCTTGAAGAAATGTGCGGACAGATCCCTTAACAA	1020
Db	2176	GTGCTGAAGAAAGGAATTAACACCATCTTGAAGAAATGTGCGGACAGATCCCTTAACAA	2235
QY	1021	GGCACACTCCCTAGGCCCCCTGTGCTCCATCGTGCACCGAGGCCCCCAAGCCGAGT	1080
Db	2236	GGCACACTCCCTAGGCCCCCTGTGCTCCATCGTGCACCGAGGCCCCCAAGCCGAGT	2295
QY	1081	CTTCCAAAGCTCTCTCTCATATGATCAAGAGGCTGACAGTGGCCTGTGCTTCCCGGTG	1140
Db	2296	CTTCCAAAGCTCTCTCTCATATGATCAAGAGGCTGACAGTGGCCTGTGCTTCCCGGTG	2355

1141 AATGCTCTGCTGATCTGAGCTGAGAGCTCTTGCTCCAGGCTCCAGAAAGAAATGG 1200  
2356 AATGCTCTGCTGATCTGAGCTGAGAGCTCTTGCTCCAGGCTCCAGAAAGAAATGG 2415  
1201 AGAGGGAACTAGCTTAAGGGAATCTGAGGGGACAGGTTTCTTCCAGAGGAAAGG 1260  
2416 AGAGGGAACTAGCTTAAGGGAATCTGAGGGGACAGGTTTCTTCCAGAGGAAAGG 2475  
1261 GCCTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGACAGGAGTGGGACGCTGGAGC 1320  
2476 GCCTCCAGCTCCAGAGAAATTCAGAGAGTGGGACCTGACAGGAGTGGGACGCTGGAGC 2535  
1321 TGAGCGGCTGCTGAAGAGCAGAAAGTGAAGGAGGAGGCTGAAGCTGACAGTTC 1380  
2536 TGAGCGGCTGCTGAAGAGCAGAAAGTGAAGGAGGAGGCTGAAGCTGACAGTTC 2595  
1381 AGTGTGTTCACGGGGCTGGGAGTTTCCGTTGCTTCCGTGAGCCCTTTTATCTTTCT 1440  
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1441 CTGCTTGAGAGAGAAAGCTATTTCAATGAAGGAGTGCAGTTCAATGAAGTCAAGCTGT 1500  
2656 CTGCTTGAGAGAGAAAGCTATTTCAATGAAGGAGTGCAGTTCAATGAAGTCAAGCTGT 2715  
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2776 GAAGCGAGCTATTTCTTAGGCGCTTAATTCAGGAAAGTGAAGTGAAGTCTTTTCTTT 2835  
1621 CATGCTTCTGAGCACTACTCAGCCCTGAGTGAAGTGGCTTATGCAAGAGGTCGA 1680  
2836 CATGCTTCTGAGCACTACTCAGCCCTGAGTGAAGTGGCTTATGCAAGAGGTCGA 2895  
1681 AACCTTGAATCAGAGAGCTCGGTTTCTTCTGTTCTGCAATGAGTGGCTGTCGAC 1740  
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3016 GCTCTGCTGTTCTGTAACACTTCCCTGATTCCTGTAAGGGGGAGTGAAGGGG 3075  
1861 AAGAGGCAAGCTGAGAGCTGAGCAAGAGGAGTGAAGGGGAGAGAGGCAAG 1920  
3076 AAGAGGCAAGCTGAGAGCTGAGCAAGAGGAGTGAAGGGGAGAGAGGCAAG 3135  
1921 CAGAACTGGTCTCATCACTGCTCACTGATCACTCAAGCTCAGAGCCGAGAGCA 1980  
3136 CAGAACTGGTCTCATCACTGCTCACTGATCACTCAAGCTCAGAGCCGAGAGCA 3195  
1981 CAATGCTTCAAGAAAGCTGAATGAACCAAGCCCAATTTTCTTCCCTTAAGCATAGC 2040  
3196 CAATGCTTCAAGAAAGCTGAATGAACCAAGCCCAATTTTCTTCCCTTAAGCATAGC 3255  
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3256 AATGGCAATTTGCAATTAACCAAAAGATGAGAGACTAAGTGGTACGTTTTCGCG 3315  
2101 GCAATCAAAAATCTGGGCGCAGAGAGTGAATAATGCCAGAGTGTAAATCTTTTCAACC 2160  
3316 GCAATCAAAAATCTGGGCGCAGAGAGTGAATAATGCCAGAGTGTAAATCTTTTCAACC 3375  
2161 TGAGCGAGCCCAAGCAGCTGAGAGTGAAGTGTGACAGCAGAGTGAAGTGTGACGCG 2220  
3376 TGAGCGAGCCCAAGCAGCTGAGAGTGAAGTGTGACAGCAGAGTGAAGTGTGACGCG 3435  
2221 AGGGAGAGAAAGAAAGAGAGGAGTATGTATGAGCAAGAAAGACAGATTCATTCAG 2280

3436 AGGGAGAGAAAGAAAGAGAGGATAGTATGAGCAAGAAAGACAGATTCATTCAG 3495  
2281 GGAAGGGAATTTAGCAAGGATTAATGCTCAGCTGATCTCGGTTCTAGAGGAGG 2340  
3496 GGAAGGGAATTTAGCAAGGATTAATGCTCAGCTGATCTCGGTTCTAGAGGAGG 3555  
2341 GCTAATTTGAGGGGAGAAATCAGTCAAGGAAAGTGGGAGCTGATTTCTAATTC 2400  
3556 GCTAATTTGAGGGGAGAAATCAGTCAAGGAAAGTGGGAGCTGATTTCTAATTC 3515  
2401 TATATTTTCTTTCAAGCTGATTAATCTGACAGTCAAGGATTAATCTGAGGCT 2460  
3616 TATATTTTCTTTCAAGCTGATTAATCTGACAGTCAAGGATTAATCTGAGGCT 3675  
2461 GTAAATTAATTAATTTCTCTTATTAAGAACTTTTCTCTGAGTGAAGCAGCA 2520  
3676 GTAAATTAATTAATTTCTCTTATTAAGAACTTTTCTCTGAGTGAAGCAGCA 3735  
2521 AGGGCAATCCGTTCTTTTACAGGAAAGAAATCTCTAAGTAAAGCCAAAGAT 2580  
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2581 TCAAGCTAGTCTTCTGCTGACTATATGATGGTTTGAAGAAATCAATTCAGCGAT 2640  
3796 TCAAGCTAGTCTTCTGCTGACTATATGATGGTTTGAAGAAATCAATTCAGCGAT 3855  
2641 TACTATCTGATTAAGAAATGAGACTAGTACCCTTTGTCAGCTGAACCAACCCAT 2700  
3856 TACTATCTGATTAAGAAATGAGACTAGTACCCTTTGTCAGCTGAACCAACCCAT 3915  
2701 TTGTAAGTCTCAAGTCAAGCTTAATCTGAGAAACCAATCAATTAAGAAATCTTT 2760  
3916 TTGTAAGTCTCAAGTCAAGCTTAATCTGAGAAACCAATCAATTAAGAAATCTTT 3974  
2761 AGAGCAACTGTTCTTCCAC-TCGAGAGTGAAGTCTGACAGGCAAGTGAATAT 2819  
3975 AGAGCAACTGTTCTTCCACATGAGAGTGAAGTCTGACAGGCAAGTGAATAT 4034  
2820 TACTTCAAGATTAAGCACTGTTGATTAACAATTAAGTGTCTCAAGGCAAT 2879  
4035 TACTTCAAGATTAAGCACTGTTGATTAACAATTAAGTGTCTCAAGGCAAT 4094  
2880 CATTAATCAAGTCTTAAGTACTCTGACATTTTGTGAATTAATGGCATTC 2939  
4095 CATTAATCAAGTCTTAAGTACTCTGACATTTTGTGAATTAATGGCATTC 4154  
2940 CATTTGCTTTTGTCTTCTTGGTTTATTAATGAAGAGGATTAATTAACCTA 2999  
4155 CATTTGCTTTTGTCTTCTTGGTTTATTAATGAAGAGGATTAATTAACCTA 4214  
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3060 TCTAATTAATTAATTTTATTTGCAATTTGGAATGAAGCCATTAATCAAGTGAAT 3119  
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3120 AACAGTACCTGATTTTGTCAATTAACAATGAATCAAGACATTTATTAATTAAT 3179  
4335 AACAGTACCTGATTTTGTCAATTAACAATGAATCAAGACATTTATTAATTAAT 4394  
3180 AGTGTTCAGATGCTTGAATGAATTAATTAATTAATTAATTAATTAATTAAT 3239  
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3240 CTCCTGAGATCTTGTTTTAATTAATTAATTAATTAATTAATTAATTAATTTG 3299  
4455 CTCCTGAGATCTTGTTTTAATTAATTAATTAATTAATTAATTAATTAATTTG 4514  
3300 ATTAATCAATTAATTAATTAATTTGTTCTTGTGAATTAATTAATTAATTAATTAAT 3359

D	b		4515	A T A A T C A A T T A C T A T A T C A A T T G T T C C T T G T A A T C T A A T T T A T A T T T A A T T G A A A C	4574
O	y		3360	A T C T T T C T G A A A G A G T T C C C A G A T T T C A C C A A T G A G T T C T T G G A T G C A C A C A C A	3419
D	b		4575	A T C T T T C T G A A A G A G T T C C C A G A T T T C A C C A A T G A G T T C T T G G A T G C A C A C A C A	4634
O	y		3420	G A G T A A G A A C T G A T T T A G A G G C T A A C A T T G A C A T T T G G C C T G A T G C A A G A C T G A A T	3479
D	b		4635	G A G T A A G A A C G A T T T A G A G G C T A A C A T T G A C A T T T G G C C T G A T G C A A G A C T G A A T	4694
O	y		3480	T A G A A A G T T C T C C C A A A G A T A C A C A G T T G T T T A A A G C T A G A G G T G A G G G G G A A A T C T G	3539
D	b		4695	T A G A A A G T T C T C C C A A A G A T A C A C A G T T G T T T A A A G C T A G A G G T G A G G G G G A A A T C T G	4754
O	y		3540	C C G C T T C T A T A A G A A T G C T T C C C T G A G C C T G A G G T G C T G T C C T T G T T G T C G G C T	3599
D	b		4755	C C G C T T C T A T A A G A A T G C T T C C C T G A G C C T G A A G G G T G C T G T C C T T G T T G T C G G C T	4814
O	y		3600	G G C G T T A T T T T T C T G T C C C C T G C T A G T C T T A A A A G A C T T G T T G A A T C C A A G T T C C	3659
D	b		4815	G G C G T T A T T T T T C T G T C C C C T G C T A G T C T T A A A A G A C T T G T T G A T T C C A A G T T C C	4874
O	y		3660	T A G C A T A G T G C C T G G C A G A G T G A G G T T C T C A A T A G A T T T G C A G A G T A A T G A A A T A T A	3719
D	b		4875	T A G C A T A T G C C T G G C A G A G T G A G G T T C T C A A T A G A T T T G C A G A G T A A T G A A A A T A T A	4934
O	y		3720	A A C T A G A A A T A T A T C T T T G T T G A A A T C A C A C A C A G T A G T C T G T G T A A T G T G T G T A	3779
D	b		4935	A A C T A G A A A T A T A T C T T T G T T G A A A T C A C A C A C A G T A G T C T G T G T A A T G T G T G T A	4994
O	y		3780	C - G T G T G T G T G T G T G T G T G T G T G T G T A A A C C A G G T G A G A N T A T G A A C T A T A T T	3837
D	b		4995	C G T G T G T G T G T G T G T G T G T G T G T G T A A A C C A G G T G A G A N T A T G A A C T A T A T T	5054
O	y		3838	G G G G T A T G G G T G C A T A A A T G G G A T G T T C T T T T A A A A A A A A C T C A A A C A G A C T T C T G	3897
D	b		5055	G G G G T A T G G G T G C A T A A A T G G G A T G T T C T T T T A A A A A A A A C T C A A A C A G A C T T C T G	5114
O	y		3898	G A A G G T A T T T T C T A A G A A T C T T G C T G C A G G C T G A A G G C A A C C C C C T G T G C A C A G C C	3957
D	b		5115	G A A G G T A T T T T C T A A G A A T C T T G C T G C A G G C T G A A G G C A A C C C C C T G T G C A C A G C C	5174
O	y		3958	C A C C A G C C T C A C G T G G C A C C T C T G T C T T C C C C A T G A A G G G C T G G C T C C C C A G T A A T	4017
D	b		5175	C A C C A G C C T C A C G T G G C A C C C T C T G T C T T C C C C A T A A G G G C T G G C T C C C C A G T A A T	5234
O	y		4018	A T A A A C T C T C G A G A C T C A G G C A T G A G G C A G A G G C A C C C A T C A G A G G C A C C T C T A G	4077
D	b		5235	A T A A A C T C T C G A G A C T C G G S C A T G A G C A G A A G G C A C C C A T C A G A G G C A C C T C T A G	5294
O	y		4078	C A C A G C A G A G C T T T C C A G A G A A G C C T C A C C A A G C C T C T G C A A T A G G T T C T T C T G T G C A	4137
D	b		5295	C A C A G C A G A G C T T T C C A G A G A A G C C T C A C C A A G C C T C T G C A A T A G G T T C T T C T G T G C A	5354
O	y		4138	C G T T G C T G C A G C T T T G G G C C T G A A T G C A G C T G T C A G C T G C T T C T T G G C C T G C C T G	4197
D	b		5355	C G T T G C T G C A G C T T T G G G C C T G A A T G C A G C T G T C A G C T G C T T C T T G G C C T G C C T G	5414
O	y		4198	G T G T G G A A T G T G G G G G C A G A G A G C T A G C T C A G A A A G G C C A A T G A C C A A G T G G C C G A	4255
D	b		5415	G T G T G G A A T G T G G G G G C A G A A G C T A G C T C A G A A A G G C C A A T G A C C A A G T G G C C G A	5474
O	y		4258	T G C A G T A T A C C T T C A G T G T G G C A G T C C C A A T G A A T C C A G C T G C C A G A G C A G A C C A G	4317
D	b		5475	T G C A G T A T A C C T T C A G T G T G G C A G T C C C A A T G A A T C C A G C T G C C A G A G C A G A C C A G	5533
O	y		4318	G C C A T T C A G T C A T C A T A C T T T A C A G A G A C A G A G C A C C C A A C G C T T A G A C C T G A G	4377
D	b		5535	G C C A T T C A G T C A T C A T A C T T T A C A G A G A C A G A G C A C C C A A C G C T T A G A C C T G A G	5599
O	y		4378	G C C A C C A A A G C T G A A T C A G C T C C C T G A G A G A C C T C T C A C A A T T A C C T T T G A C C A G	4433
D	b		5595	G C C A C C A A A G C T G A A T C A G C T C C C T G A G A G A C C T C T C A C A A T T A C C T T T G A C C A G	5655

QY	4438	GCTCCACGACCCCGGAGAGACCCAGAGAGAGGCGCTGCGAGAGGAGCGTGGGCAACCTGTAAGGCGG	4497
Db	5555	GCTCCACGAGGCCCCCAGAGAGACCCAGAGAGAGGCGCTGCGAGAGAGCGCTGGGCAACCTGTAAGGCGG	5714
QY	4498	GAGCGGAGACCGAGCTGAGAAACCCAAACAGAGAGTTGGAGACTGCTCAGCAACCTCCTC	4557
Db	5715	GAGCGGAGACCGAGCTGAGAAACCCAAACAGAGAGTTGGAGACTGCTCAGCAACCTCCTC	5774
QY	4558	CGAGACAAAGTCAGTTCTGGAGAGAAAGAGAGCGACTAAGGCGAAGAAATGAGATCTG	4617
Db	5775	CGAGACAAAGTCAGTTCTGGAGAGAAAGAGAGCGACTAAGGCGAAGAAATGAGATCTG	5834
QY	4618	GCCAGAGAGTTGGAGAAACGAGAGCGCAGAGAGGTAGCAAGCGCTGAGAAAGGCGCAGTGTCC	4677
Db	5835	GCCAGAGAGTTGGAGAAACGAGAGCGCAGAGAGGTAGCAAGCGCTGAGAAAGGCGCAGTGTCC	5894
QY	4678	CAGACCCGAGACACTGCTCGGCGCTGTGCGACCAAGCGCTCCAGAGAGAGGTAAAGATGAGAG	4737
Db	5895	CAGACCCGAGACACTGCTCGGCGCTGTGCGACCAAGCGCTCCAGAGAGAGGTAAAGATGAGAG	5954
QY	4738	TGGGGGGAGCTCTGAGTTGAGAGAGTGAATATGGCTCTGATGTAACCTGCTACAGGCGCTCCA	4797
Db	5955	TGGGGGGAGCTCTGAGTTGAGAGAGTGAATATGGCTCTGATGTAACCTGCTACAGGCGCTCCA	6014
QY	4798	GGCCCTCCCTGCGTGGCCCTTCTCCTAGAGACTGCGACAGCTAGCACAAGACAGATGATTA	4857
Db	6015	GGCCCTC---CCTGCCCTTCTCCTAGAGACTGCGACAGCTAGCACAAGATGATTA	6070
QY	4858	AGGAAGCAGACCGATCACCTTCAAGTATTACTAGTAATTTAGTCTCTGAGAGCTTCAT	4917
Db	6071	AGGAAGCACA-CGATCACCTTCAAGTATTACTAGTAATTTAGTCTCTGAGAGCTTCAT	6129
QY	4918	TAGATTAGTGTTCAGAGCTTCGTGGCCCTCCATGTCAG	4957
Db	6130	TAGATTAGTGTTCAGAGCTTCGTGGCCCTCCATGTCAG	6169
RESULT 3			
US-08-938-669A-1			
/ Sequence 1, Application US/08938669A			
/ Patent No. 6171788			
/ GENERAL INFORMATION:			
/ APPLICANT: Nguyen, Thai D.			
/ TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,			
/ TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND			
/ TITLE OF INVENTION: RELATED DISEASES			
/ NUMBER OF SEQUENCES: 32			
/ CORRESPONDENCE ADDRESS:			
/ ADDRESSEE: Howrey & Simon			
/ STREET: 1299 Pennsylvania Avenue, N.W.			
/ CITY: Washington			
/ STATE: DC			
/ COUNTRY: USA			
/ ZIP: 20004-2402			
/ COMPUTER READABLE FORM:			
/ MEDIUM TYPE: Diskette			
/ COMPUTER: IBM Compatible			
/ OPERATING SYSTEM: DOS			
/ SOFTWARE: FASTSEQ for Windows Version 2.0			
/ CURRENT APPLICATION DATA:			
/ APPLICATION NUMBER: US/08/938,669A			
/ FILING DATE:			
/ CLASSIFICATION: 435			
/ PRIOR APPLICATION DATA:			
/ APPLICATION NUMBER: 08/791,154			
/ FILING DATE: 28-JAN-1997			
/ ATTORNEY/AGENT INFORMATION:			
/ NAME: Mendelson, Elliot			
/ REGISTRATION NUMBER: P-42,878			
/ REFERENCE/DOCKET NUMBER: 07425-0034			
/ TELECOMMUNICATION INFORMATION:			

RESULT 3  
US-08-938-669A-1

; Sequence 1, Application US/08938669A  
; Patent No. 6171788

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; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
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APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR

TITLE OF INVENTION:	PROGNOSIS AND
TITLE OF INVENTION:	RELATED DISEASE
;	;

; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Ave

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;
; CITY: Washington
; STATE: DC

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; COUNTRY: USA
; ZIP: 20004-2402
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FASTSEQ FOR WINDOWS
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/938,  
FILING DATE:

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot

REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 0742;

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 383-6857  
 ; TELEFAX: 202 383-6610  
 ;  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5300 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ;  
 US-08-938-669A-1

Query Match 67.8%; Score 4069.4; DB 3; Length 5300;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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QY      61 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTATGCTCTACACCTGAGCTCACTGC 120
DB      1276 CGTAGAGGTGAGGGTCTGTCTTACACCTACCTATGCTCTACACCTGAGCTCACTGC 1335
QY      121 AACCTTGCTCTCCAGGTTCAAGCAATTCCTGTCTCAGCCTCCGCGTAGCTGGACT 180
DB      1336 AACCTTGCTCTCCAGGTTCAAGCAATTCCTGTCTCAGCCTCCGCGTAGCTGGACT 1395
QY      181 AAGAGGCGACGCCCGGCTAATTTTGTATTGTTAGTAGAGAGGGGTTTACCATATTAG 240
DB      1396 AAGAGGCGACGCCCGGCTAATTTTGTATTGTTAGTAGAGAGGGGTTTACCATATTAG 1455
QY      241 CCCGGCTGCTTGAACCTCTGACCTCAGATGATCCACCACTCAGCCTCCCTAAAGTGC 300
DB      1456 CCCGGCTGCTTGAACCTCTGACCTCAGATGATCCACCACTCAGCCTCCCTAAAGTGC 1515
QY      301 TGGGATTACAGGATGATGACCGCGCGCCGCAAGGGTCACTGTTTAAAGAAATAC 360
DB      1516 TGGGATTACAGGATGATGACCGCGCGCCGCAAGGGTCACTGTTTAAAGAAATAC 1575
QY      361 TTGANTGGTTTACTAAACCAACAGGAAACAGCAAAAGCTGTGATATTTCAGGGATTG 420
DB      1576 TTGANTGGTTTACTAAACCAACAGGAAACAGCAAAAGCTGTGATATTTCAGGGATTG 1635
QY      421 TTGGATGGGGAATGATGCTGATGAGCTGCTGCTAGTCCAGACCACTGCTCATATCA 480
DB      1636 TTGGATGGGGAATGATGCTGATGAGCTGCTGCTAGTCCAGACCACTGCTCATATCA 1695
QY      481 CTTTCTCTCCCTCATCTCAATTTTCAGGCTAAGTTACATTTTATTCACCATCTTTTGTG 540
DB      1696 CTTTCTCTCCCTCATCTCAATTTTCAGGCTAAGTTACATTTTATTCACCATCTTTTGTG 1755
QY      541 GTAACCTTCACATGTTACTGAATTAAGATTAATCAATTAATGATTCATTTGGGGCCA 600
DB      1756 GTAACCTTCACATGTTACTGAATTAAGATTAATCAATTAATGATTCATTTGGGGCCA 1815
QY      601 TCTGTGTGTGTATAGGGGAGAGGGGCAATACCCAGAGACTCTTTGAAGCCCGGGGAG 660
DB      1816 TCTGTGTGTGTATAGGGGAGAGGGGCAATACCCAGAGACTCTTTGAAGCCCGGGGAG 1875
QY      661 AGGTTTCTCTTCAGCTGGGGAGGCTGTGCAAGACCCGGGGTCTGTGGTGTCTGAGACA 720
DB      1876 AGGTTTCTCTTCAGCTGGGGAGGCTGTGCAAGACCCGGGGTCTGTGGTGTCTGAGACA 1935
QY      721 ACCTCGAGCCCGGTGCCACTGTGTGTTTGTATTAACAATCTTAAGGACCTGTGCTTTCT 780
DB      1936 ACCTCGAGCCCGGTGCCACTGTGTGTTTGTATTAACAATCTTAAGGACCTGTGCTTTCT 1995
QY      781 ATTTCGTGTGACTGTTCAATTCATCAAGGACTTCAATTAACAATTAATTAAGTACTATA 840
DB      1996 ATTTCGTGTGACTGTTCAATTCATCAAGGACTTCAATTAACAATTAATTAAGTACTATA 2055
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DB      2116 GTGACAGTTTCTCAGAGAGAGTGTGACAGAAATTAATTAACCGCACTTAAACCA 2175
QY      961 GTGCTGAAGAAAGAAATTAACCAATCTTGAAGATTGTGCGAGACATCCCTTAACA 1020
DB      2176 GTGCTGAAGAAAGAAATTAACCAATCTTGAAGATTGTGCGAGACATCCCTTAACA 2235
QY      1021 GGCACCTTCCTAGGCCCCCTGCTGCTCATATGTCGCCGAGGCCCCCAAGCCGAGT 1080
DB      2236 GGCACCTTCCTAGGCCCCCTGCTGCTCATATGTCGCCGAGGCCCCCAAGCCGAGT 2295
QY      1081 CTTCCAGCTCTCTCTCATATGTCACAGGCTGCAAGCTGAGCTGCTCGCTTCCTG 1140
DB      2296 CTTCCAGCTCTCTCTCATATGTCACAGGCTGCAAGCTGAGCTGCTCGCTTCCTG 2355
QY      1141 AATGCTCTGCTGATCTGAGCTGAGACTCCTTGCTCCAGGCTCCAGAAAGAAATAG 1200
DB      2356 AATGCTCTGCTGATCTGAGCTGAGACTCCTTGCTCCAGGCTCCAGAAAGAAATAG 2415
QY      1201 AAGGGAATAGTCTAAAGAGATCTGAGGGGACATGTTTCTCAGAGGAAAGG 1260
DB      2416 AAGGGAATAGTCTAAAGAGATCTGAGGGGACATGTTTCTCAGAGGAAAGG 2475
QY      1261 GCTCCACGTCCAGAGAAATTCAGAGAGTGGGACCTGACGGAAGTGGGACGCTGGGC 1320
DB      2476 GCTCCACGTCCAGAGAAATTCAGAGAGTGGGACCTGACGGAAGTGGGACGCTGGGC 2535
QY      1321 TGAGGGGTGTGAAAGGACAGGAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 1380
DB      2536 TGAGGGGTGTGAAAGGACAGGAAGTGAAGAAAGGCTGAAGCTGCCAGATGTC 2595
QY      1381 AGTGTGTTCAAGGGGCTGGAGATTTCCTGTGCTCTCTGAGAGCTTTTATCTTTCT 1440
DB      2596 AGTGTGTTCAAGGGGCTGGAGATTTCCTGTGCTCTCTGAGAGCTTTTATCTTTCT 2655
QY      1441 CTGCTTGAAGAGAAAGATCTAATTTCAATGAAGGATCAGTTTCAATTAAGTCACTGTT 1500
DB      2656 CTGCTTGAAGAGAAAGATCTAATTTCAATGAAGGATCAGTTTCAATTAAGTCACTGTT 2715
QY      1501 AAAATTCAGAGGTGATGAGGTTTTCCTTCAAGAGGCTTTAATTAATGGAAATAG 1560
DB      2716 AAAATTCAGAGGTGATGAGGTTTTCCTTCAAGAGGCTTTAATTAATGGAAATAG 2775
QY      1561 GAAGGAGCTAATTTCTAGGCGCTTAATTCACGGAAGATGAATGAGTCTTTCTTT 1620
DB      2776 GAAGGAGCTAATTTCTAGGCGCTTAATTCACGGAAGATGAATGAGTCTTTCTTT 2835
QY      1621 CATGCTTTGGGCACTAATCTAGGCTGTGTGATCTGAGCTTAATGCAAGCGTGGAA 1680
DB      2836 CATGCTTTGGGCACTAATCTAGGCTGTGTGATCTGAGCTTAATGCAAGCGTGGAA 2895
QY      1681 AACCTGGAATCAGAGACTGAGTTTCTTCTGCTTGTGCAATGCTGTGCTGTGCGAC 1740
DB      2896 AACCTGGAATCAGAGACTGAGTTTCTTCTGCTTGTGCAATGCTGTGCTGTGCGAC 2955
QY      1741 CGTGGCAAGTGTCTCTCTCCCTGAGCAATGATCTTCTGTGTAATGAACCTTTGCA 1800
DB      2956 CGTGGCAAGTGTCTCTCTCCCTGAGCAATGATCTTCTGTGTAATGAACCTTTGCA 3015
QY      1801 GCTCTCGTGTCTGTGAACATTCCTCTGTGATTTCTGTGAGGGGGATGTTGAGAGGG 1860
DB      3016 GCTCTCGTGTCTGTGAACATTCCTCTGTGATTTCTGTGAGGGGGATGTTGAGAGGG 3075
QY      1861 AAGGAGGAGAGCTGAGAGCTGAGCCACGAGGCAAGGGAGGTGAGGGGACAGGAAGGACG 1920
DB      3076 AAGGAGGAGAGCTGAGAGCTGAGCCACGAGGCAAGGGAGGTGAGGGGACAGGAAGGACG 3135
QY      1921 CAGAAGCTGGGTGTCTCATAGTCTCATCTGATCACTGATCACTCAAGACCGAGAGCCA 1980
DB      3136 CAGAAGCTGGGTGTCTCATAGTCTCATCTGATCACTGATCACTCAAGACCGAGAGCCA 3195
  
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Oy	1381	CAAGGCTTCAGGAAAGCTGCATGAAACCCAA	CAGGCA	CATTTCCTCCCTTAACATAGAC	2040		
Db	3196	CAATGCTTCAGGAAAGCTCAATGAAACCCAA	CAGGCA	CATTTCCTCCCTTAACATAGAC	3255		
Oy	2041	AATGGCATTTGGCCAAATACCAAAAAAGATG	CAGAGCTAA	CTGGTGGTAGCTTTTCCTG	2100		
Db	3256	AATGGCATTTGGCCAAATACCAAAAAAGATG	CAGAGCTAA	CTGGTGGTAGCTTTTCCTG	3315		
Oy	2101	GCATTTCAAAAACTGGGCCAAGGCAAGTGGA	AAAAACGAGAT	TTGTTAACTTTTCAACC	2160		
Db	3316	GCATTTCAAAAACTGGGCCAAGGCAAGTGGA	AAAAACGAGAT	TTGTTAACTTTTCAACC	3375		
Oy	2161	TGACCAGACCCCA	CGCAGCTCAGCAGTGA	CTGCTGACAGCAGAGTGA	CTGCAAGCG	2220	
Db	3376	TGACCAGACCCCA	CGCAGCTCAGCAGTGA	CTGCTGACAGCAGAGTGA	CTGCAAGCG	3435	
Oy	2221	AGGGAGGAGAAAGAAAAAGAGGGAATG	TGTGTATGACAGAAAGACAGATTC	TTCAAG	2280		
Db	3436	AGGGAGGAGAAAGAAAAAGAGGGAATG	TGTGTATGACAGAAAGACAGATTC	TTCAAG	3495		
Oy	2281	GGCAGTGGGAATTGACCA	CAGGAAATTATG	CCACGATCTCGGCTTTAGAGAGG	CAGG	2340	
Db	3496	GGCAGTGGGAATTGACCA	CAGGAAATTATG	CCACGATCTCGGCTTTAGAGAGG	CAGG	3555	
Oy	2341	GCTATATTGTGGGGGAAAAAATCAGTTCA	GAGGAAGTCGGGAG	ACTGATTTCTAATAC	2400		
Db	3556	GCTATATTGTGGGGGAAAAAATCAGTTCA	GAGGAAGTCGGGAG	ACTGATTTCTAATAC	3615		
Oy	2401	TATATTTTCTCTTTACAA	GCTGAGTAATTTTGACAGAA	GTCA	CAGGTAATGTA	CTGAGGCT	2460
Db	3616	TATATTTTCTCTTTACAA	GCTGAGTAATTTTGACAGAA	GTCA	CAGGTAATGTA	CTGAGGCT	3675
Oy	2461	GTAAGATTACTTAGTTTCT	CCCTATTAGGA	CTCTTTTCTCTGAGAGTTAG	CAGACA	2520	
Db	3676	GTAAGATTACTTAGTTTCT	CCCTATTAGGA	CTCTTTTCTCTGAGAGTTAG	CAGACA	3735	
Oy	2521	AGGGCAATCCGGTCTTTTAA	CAGGAAGAAACATTC	TAAAGTAAGCCAAAC	CAAT	2580	
Db	3736	AGGGCAATCCGGTCTTTTAA	CAGGAAGAAACATTC	TAAAGTAAGCCAAAC	CAAT	3795	
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Db	3796	TCAAACCTAAGGCTTGCTG	ACATATGATTTGGTTTTGAA	AAATCA	TTTCAGGAGATGT	3855	
Oy	2641	TACTATCTGATTCAGAAAA	TAGAGACTAGTAC	CCTTTGGCTGTAA	CAAAACCCAT	2700	
Db	3856	TACTATCTGATTCAGAAAA	TAGAGACTAGTAC	CCTTTGGCTGTAA	CAAAACCCAT	3915	
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Db	3916	TTGTAAATGTC	CAAGTTCAAGGCTTA	ACTGCAGAACCAATCA	ATTAATGAATCTTT	3975	
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Db	3976	AGAGCAAACTG	GTGTTCTCAACTG	AGAGTGA	GTCTGCAGGCGCAGTTTGGAA	ATATTT	4035
Oy	2821	ACTTCACAAGTATG	ACACTGTGTGGTATTA	CAACATTAAGTTG	CTCAAGGCAATC	2880	
Db	4036	ACTTCACAAGTATG	ACACTGTGTGGTATTA	CAACATTAAGTTG	CTCAAGGCAATC	4095	
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Db	4096	ATTATTTCAAGGCGCTAA	AGTACTCTG	ACAGTTTGGTAATTA	ATGSGCATTTGCC	4155	
Oy	2941	ATTTCCTTTTGTGTTTTCT	CTTTGGGTTATTA	TGTAAAGCAGGGA	TTATTAACCTAC	3000	
Db	4156	ATTTCCTTTTGTGTTTTCT	CTTTGGGTTATTA	TGTAAAGCAGGGA	TTATTAACCTAC	4215	
Oy	3001	AGTCCAGAAAGCCTG	TGAATTTGAATAG	AGAAAAATTA	CAATTTTGTGTTTTAC	CTT	3060
Db	4216	AGTCCAGAAAGCCTG	TGAATTTGAATAG	AGAAAAATTA	CAATTTTGTGTTTTAC	CTT	4275

QY	3061	CTAACTAAATTTAACATTTTATTCATTGGAAATAGAGCCATAAATCAAAGGGTATA	3120
Db	4276	CTAACTAAATTTAACATTTTATTCATTGGAAATAGAGCCATAAATCAAAGGGTATA	4335
QY	3121	ACAGTACCTGATTTTGTGATTCACATAGAAATCAAGACATTTATCTATTTACA	3180
Db	4336	ACAGTACCTGATTTTGTGATTCACATAGAAATCAAGACATTTATCTATTTACA	4395
QY	3181	GTTGTGCAGATACGTTGTGAAGTGAATATTATATCTCAAAATCTACTTTGAAATTAGCC	3240
Db	4396	GTTGTGCAGATACGTTGTGAAGTGAATATTATATCTCAAAATCTACTTTGAAATTAGCC	4455
QY	3241	TCTGCTGAGATCTGTTTTTAACATATTAATAAAACATGTTAAATTTTGATTTTGA	3300
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QY	3301	TAAATCATTTTCATTTATCATTTGTTTCTCTTGTAATCTAATATTTATATTTGAAAAA	3360
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QY	3361	TCTTTCTGAGAAAGTTCCCAAGATTTCAACCAATGAGGTTCTTGACATGCACACACAG	3420
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QY	3421	AGTAAGAACTGATTTTAAAGGCTAACATTTGAATGTGTGCTGAGATGCAACATGGAATT	3480
Db	4636	AGTAAGAACTGATTTTAAAGGCTAACATTTGAATGTGTGCTGAGATGCAACATGGAATT	4695
QY	3481	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAATCTGC	3540
Db	4696	AGAAAGTTCTCCCAAGATACACAGTTGTTTAAAGCTAAGGGGTGAGGGGGGAATCTGC	4755
QY	3541	CGCTTCTATAGGAATGCTCTCCCTGAGACCTGTAGGGTGTGCTTGTGTTCTGCGCTG	3600
Db	4756	CGCTTCTATAGGAATGCTCTCCCTGAGACCTGTAGGGTGTGCTTGTGTTCTGCGCTG	4815
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Db	4816	GCTGTAAATTTTTCTCTGTCCCTGCTACGTCTTAAAGAACTTGTTGATCTCCAGTTCT	4875
QY	3661	ACCATAGGCCCTGGACAGTGAAGGTTCTCATGATGTTGCAAGTGAATGGAATATATA	3720
Db	4876	ACCATAGGCCCTGGACAGTGAAGGTTCTCATGATGTTGCAAGTGAATGGAATATATA	4935
QY	3721	ACTAGAAATATATCTCTTGTTGAATACAGACACACAGTAGTCTGTGTGAATGTGTAC	3780
Db	4936	ACTAGAAATATATCTCTTGTTGAATACAGACACACAGTAGTCTGTGTGAATGTGTAC	4995
QY	3781	- -GTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAAGATATAGAACTATATTG	3833
Db	4996	- -GTGTGTGTGTGTGTGTGTGTGTGTAAACCAAGTGAAGATATAGAACTATATTG	5055
QY	3833	GGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGG	3898
Db	5056	GGGTATGGGTGATTAATTTGGGATGTTCTTTTAAAGAACTCCAAACAGACTTCTGG	5115
QY	3899	AAGGTATTTTCTAAGAACTTGCTGCGCAGCGTGAAGGCAACCCCTGTGCAACAGCCC	3958
Db	5116	AAGGTATTTTCTAAGAACTTGCTGCGCAGCGTGAAGGCAACCCCTGTGCAACAGCCC	5175
QY	3959	ACCCAGCCTCAAGTGGCCACTGTGTCTTCCCAATGAAGGGCTGCTCCCAATATATA	4018
Db	5176	ACCCAGCCTCAAGTGGCCACTGTGTCTTCCCAATGAAGGGCTGCTCCCAATATATA	5233
QY	4019	TAAACTCTCTGAGCTCAGGCAATGACCAAGCAAGCCCAATCCAGGCACTCTCAGC	4076
Db	5236	TAAACTCTCTCTGAGCTCTGGGCAATGAGCCAGCAAGCCCAATCCAGGCACTCTCAGC	5295
QY	4079	ACAGC 4083	
Db	5296	ACAGC 5300	

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RESULT 4
US-09-306-828-1
; Sequence 1, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; EARLIER FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-1

Query Match      67.8%; Score 4069.4; DB 3; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY      1  GCTCCAGGAAGTCTCCCACTGACTGATTCGTGACATGATGTTACAGCCAGAAAGCTC 60
DB      1216 GCTCCAGGAAGTCTCCCACTGACTGATTCGTGACATGATGTTACAGCCAGAAAGCTC 1275
QY      61  CGTAGAGGTAGAGGTCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTACCTGC 120
DB      1276 CGTAGAGGTAGAGGTCTGTGTCTTACACCTACCTGATGCTTACACCTGAGCTACCTGC 1335
QY      121  AACCTGTGCTCCAGAGTTCAAGCAATTCTCTGTCTCAGCCTCCGCGTAGTGGAGCT 180
DB      1336 AACCTGTGCTCCAGAGTTCAAGCAATTCTCTGTCTCAGCCTCCGCGTAGTGGAGCT 1395
QY      181  ACAGGCGACGCGCGGCTAATTTTGTATTTGATGATGATGAGATGGGGTTTCAACATTTAG 240
DB      1396 ACAGGCGACGCGCGGCTAATTTTGTATTTGATGATGATGAGATGGGGTTTCAACATTTAG 1455
QY      241  CCGGCGTGTCTTGAATCTCTGACTCAGGTGATCCACCACCTCAGCCTCTTAAAGTGC 300
DB      1456 CCGGCGTGTCTTGAATCTCTGACTCAGGTGATCCACCACCTCAGCCTCTTAAAGTGC 1515
QY      301  TGGGATTAAGGCGATGATGACCGCGCCCGGCGCAAGGGTCAAGTGTAAATAGGAATTAAC 360
DB      1516 TGGGATTAAGGCGATGATGACCGCGCCCGGCGCAAGGGTCAAGTGTAAATAGGAATTAAC 1575
QY      361  TTGAATGTTTACTAATCAACAGGGAACAGACAAAGCTGTGATTAATTTACAGGATTC 420
DB      1576 TTGAATGTTTACTAATCAACAGGGAACAGACAAAGCTGTGATTAATTTACAGGATTC 1635
QY      421  TTGGGATGGGGAATGGTGCATGAGCTGCTGCTGATGCCAGAACCACTGATGCTCATCA 480
DB      1636 TTGGGATGGGGAATGGTGCATGAGCTGCTGCTGATGCCAGAACCACTGATGCTCATCA 1695
QY      481  CTTTCTTCCCTCACTCTCAATTTTCAAGGCTAAGTTACATTTTAATTCACATGCTTTTGTG 540
DB      1696 CTTTCTTCCCTCACTCTCAATTTTCAAGGCTAAGTTACATTTTAATTCACATGCTTTTGTG 1755
QY      541  GTAAGGCTCACAATGTTTACTGAATTAAGATTAATCAATTAAGTTTCAATTTTGGGGCA 600
DB      1756 GTAAGGCTCACAATGTTTACTGAATTAAGATTAATCAATTAAGTTTCAATTTTGGGGCA 1815
QY      601  TCTGTGTGTGTATATAGGGAAGAGGACATACCCAGAGACTCTTGAAGCCCGCGGAG 660
DB      1816 TCTGTGTGTGTATATAGGGAAGAGGACATACCCAGAGACTCTTGAAGCCCGCGGAG 1875
QY      661  AAGTTTCTCTCTCAGGTGAGGAGACCTTCAAGACCCGCGGGTCTTGAGTGTCTTGAGCA 720
DB      1876 AAGTTTCTCTCTCAGGTGAGGAGACCTTCAAGACCCGCGGGTCTTGAGTGTCTTGAGCA 1935
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QY      721  ACCTGCGAGCCGCTGACATGAGTGTGTTGTTATCACTCTAAGGACCTGTTGCTTCT 780
DB      1936 ACCTGCGAGCCGCTGACATGAGTGTGTTGTTATCACTCTAAGGACCTGTTGCTTCT 1995
QY      781  ATTCTGTGTGACTCGTTCATTCATTCAGGACATTCATGCAATTTATGAGTACTTATA 840
DB      1996 ATTCTGTGTGACTCGTTCATTCATTCAGGACATTCATGCAATTTATGAGTACTTATA 2055
QY      841  TCTGCCAGACACCAGACCAAAATGTTGACAAAGCATGCTACCTTCCCTTCTGTGAG 900
DB      2056 TCTGCCAGACACCAGACCAAAATGTTGACAAAGCATGCTACCTTCCCTTCTGTGAG 2115
QY      901  GTGACAGTTTCTCATGGAAGAGTGCAGAGAAATTAATTAACCGCCCACTTAAACCA 960
DB      2116 GTGACAGTTTCTCATGGAAGAGTGCAGAGAAATTAATTAACCGCCCACTTAAACCA 2175
QY      961  GTGCTGAAGAAAGAAATATAACCATCTTGAAGATTTGTGCGAGCATCTCTTAAACA 1020
DB      2176 GTGCTGAAGAAAGAAATATAACCATCTTGAAGATTTGTGCGAGCATCTCTTAAACA 2235
QY      1021  GGCACACTCTCTAGCGCCCTGTGCTCTCATTCGTGCTCCGAGAGCCCAAGCCGAGT 1080
DB      2236 GGCACACTCTCTAGCGCCCTGTGCTCTCATTCGTGCTCCGAGAGCCCAAGCCGAGT 2295
QY      1081  CTTCCAGGCTCTCTCTCATGATGATCAAGCGCTGCAAGTGGCTGCTGCTTCCCTG 1140
DB      2296 CTTCCAGGCTCTCTCTCATGATGATCAAGCGCTGCAAGTGGCTGCTGCTTCCCTG 2355
QY      1141  AATCGTCTGTGATGATGAGTGGAGACTCTTGGCTCAGGCTCCAGAAAGAAATAG 1200
DB      2356 AATCGTCTGTGATGATGAGTGGAGACTCTTGGCTCAGGCTCCAGAAAGAAATAG 2415
QY      1201  AAGAGGAAATAGTCTTAACGAGAAATCTGAGAGGAGCAAGTGTCTTCTCAGAGGAAAGG 1260
DB      2416 AAGAGGAAATAGTCTTAACGAGAAATCTGAGAGGAGCAAGTGTCTTCTCAGAGGAAAGG 2475
QY      1261  GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAGTGGGAGAGCTGGGCG 1320
DB      2476 GCTCCAGCTCCAGAGAAATTCAGAGAGTGGGAGCTGCAAGGAGTGGGAGAGCTGGGCG 2535
QY      1321  TGAGCGGCTGCTGAAGGACAGGAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 1380
DB      2536 TGAGCGGCTGCTGAAGGACAGGAAGTGAAGAAAGGCAAGGCTGAAGCTGCCAGATGTC 2595
QY      1381  AGTGTGTTCACGCGGCTGGAGATTTTCGTTGCTTCTGTGAGCCTTTTATCTTTTCT 1440
DB      2596 AGTGTGTTCACGCGGCTGGAGATTTTCGTTGCTTCTGTGAGCCTTTTATCTTTTCT 2655
QY      1441  CTGCTTGAAGAGAAAGAAAGTCTAATTTCAATGAAGGATGCAATTTCAATAAGCTGTT 1500
DB      2656 CTGCTTGAAGAGAAAGAAAGTCTAATTTCAATGAAGGATGCAATTTCAATAAGCTGTT 2715
QY      1501  AAAATTCAGGAGTGCATGAGGTTTTCCTTCAAGAAAGCCTTTAATTAATGGAATATAG 1560
DB      2716 AAAATTCAGGAGTGCATGAGGTTTTCCTTCAAGAAAGCCTTTAATTAATGGAATATAG 2775
QY      1561  GAAAGGACCTAATTTCTAGGCGCTTAATTTCAAGGAAAGTGAAGTCTTCTTCTT 1620
DB      2776 GAAAGGACCTAATTTCTAGGCGCTTAATTTCAAGGAAAGTGAAGTCTTCTTCTT 2835
QY      1621  CATGTCTTCTGGGCAACTGATCAAGCCTGTGTGTGACTTGGCTTATGCAAGCGTCA 1680
DB      2836 CATGTCTTCTGGGCAACTGATCAAGCCTGTGTGTGACTTGGCTTATGCAAGCGTCA 2895
QY      1681  AACCTTGAATCAGAGACTCGGATTTTCTTCTGAGTCTGACATGTTGTGCTGCGAG 1740
DB      2896 AACCTTGAATCAGAGACTCGGATTTTCTTCTGAGTCTGACATGTTGTGCTGCGAG 2955
QY      1741  CGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTCTGCTAATAAGACCTTTC 1800
DB      2956 CGTGGCAAGTGTCTCTCTTCCCTGGGCAATAGCTTCTCTGCTAATAAGACCTTTC 3015
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Db 5176 ACCGACCTCAGTGGCCACCTCTGTCTCCGCCCATGAGGAGCTGCCAGTATATA 5235  
QY 4019 TAAACCTCTGAGAGCTCAGGATGAGCAGCAAGCCACCATCCAGGACCTCTAGC 4078  
Db 5236 TAAACCTCTGAGAGCTCGGAGCATGAGCAGCAAGCCACCATCCAGGACCTCTAGC 5295  
QY 4079 ACAGC 4083  
Db 5296 ACAGC 5300

## RESULT 5

US-08-938-669A-2

Sequence 2, Application US/0893869A

Patent No. 6171788

GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.

APPLICANT: Polansky, Jon R.

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,

TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey &amp; Simon

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,669A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/791,154

FILING DATE: 28-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mendelson, Elliot

REGISTRATION NUMBER: P-42,878

REFERENCE/DOCKET NUMBER: 07425-0034

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 383-6857

TELEFAX: 202 383-6610

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5304 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-938-669A-2

Query Match 67.6%; Score 4057.4; DB 3; Length 5304;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 4077; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

QY 1 GCTCCACAGAGTCTCCCACTCTAGACTTGTGATGAGTGTATACAGCCAGAAAGCTC 60  
Db 1216 GCTCCACAGAGTCTCCCACTCTAGACTTGTGATGAGTGTATACAGCCAGAAAGCTC 1275  
QY 61 CGTGAAGGTGAGGAGTCTGTCTTACCACTTACTGTATGCTTACACTGAGCTCACTGC 120  
Db 1276 CGTGAAGGTGAGGAGTCTGTCTTACCACTTACTGTATGCTTACACTGAGCTCACTGC 1335  
QY 121 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTGAGCTCCCGGCTAGTGGAGCT 180  
Db 1336 AACCTCTGCTCCAGGTTCAAGCAATTCTCTGTCTGAGCTCCCGGCTAGTGGAGCT 1395

QY 181 ACAGGCGCAGCCCGGCTAATTTTGTATGTAGTAGAGATGGGGTTTCAACATATTAG 240  
Db 1396 ACAGGCGCAGCCCGGCTAATTTTGTATGTAGTAGAGATGGGGTTTCAACATATTAG 1455  
QY 241 CCCGAGCTGATCTTGAATCTCTGACCTCAGGTGATCCACACCTCCTCTAAAGTC 300  
Db 1456 CCCGAGCTGATCTTGAATCTCTGACCTCAGGTGATCCACACCTCCTCTAAAGTC 1515  
QY 301 TGGGATTACAGGATGATGATCCGCGCCGCGCAAGGTTGATGTTAATAAGAAATAC 360  
Db 1516 TGGGATTACAGGATGATGATCCGCGCCGCGCAAGGTTGATGTTAATAAGAAATAC 1575  
QY 361 TGAATGTTTACTAACCACAGGAAACAGCAAAAGCTGTAATTTTCAAGGATTC 420  
Db 1576 TGAATGTTTACTAACCACAGGAAACAGCAAAAGCTGTAATTTTCAAGGATTC 1635  
QY 421 TGGGATGGGAAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGCTCTCATCA 480  
Db 1636 TGGGATGGGAAATGGTGCATGAGCTGCTGCTAGTCCAGACCACTGCTCTCATCA 1695  
QY 481 CTTTCTTCCCTCATCTCTATTAGGCTAAGTACATTTTATTCACATGCTTTTGTG 540  
Db 1696 CTTTCTTCCCTCATCTCTATTAGGCTAAGTACATTTTATTCACATGCTTTTGTG 1755  
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QY 661 AGTTTCTCTCTCAGCTGGGAGAGCCCTGCAAGCACCGGGGCTCTGGTCTTGAAGA 720  
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Db 1936 ACCTGCAAGCCGCTGCTGCTGTTTGTATACCTCTAGGAGCCTGTGCTTCTT 1995  
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Db 2116 GTGACAGTTTCTCATGAAAGCTGCAAGAAATTAATTAAGCCCACTTAACCA 2175  
QY 961 GTGCTGAAAGAAAGAAATTAACACATCTTGAAGATTTGTCGAGCATCCCTTAACA 1020  
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 Db 3076 AAGAGGCGAGAGCTGAGAGACTGAGACCAAGAGGAGGTGAGGGGGAGAGAGAGCGAG 3135  
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 Db 3136 CAGAGGCTGGGTCTCCATCAGTCCCTCACTGATCACTGAGACTCCAGAGCCGAGAGCCA 3195  
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 Qy 2161 TGAACGACACCCCAAGCAGCTCAGAGTACTGCTGACAGCAACGAGTGAACCTGCAAGCC 2220  
 Db 3376 TGAACGACACCCCAAGCAGCTCAGAGTACTGCTGACAGCAACGAGTGAACCTGCAAGCC 3435  
 Qy 2221 AGGGAGAGAGAGAGAGAGAGAGATAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 2280  
 Db 3436 AGGGAGAGAGAGAGAGAGAGAGATAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 3495  
 Qy 2281 GGAAGTGGGAATTTGAACACAGAGATTTAGTCCACGTGATTCCTGGGTTCTAGAGAGCAGG 2340  
 Db 3496 GGAAGTGGGAATTTGAACACAGAGATTTAGTCCACGTGATTCCTGGGTTCTAGAGAGCAGG 3555  
 Qy 2341 GCTATATTGTGGGGAGAGAGAGATTCAGTTCAAGGAAGTGGGAGACCTGATTTCTAATAC 2400

Db 3556 GCTATATTGTGGGGAGAGAGAGATTCAGTTCAAGGAAGTGGGAGACCTGATTTCTAATAC 3615  
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 Db 3616 TATATTTTCTTTTACAAAGCTGAGTAATTCAGAGAGTGAACAAAGTAGTAATGAGGCT 3675  
 Qy 2461 GTAAGATTACTAGTTTCTCCCTTATTAGAACTCTTTTCTCTGTGAGTTAGCAGACA 2520  
 Db 3676 GTAAGATTACTAGTTTCTCCCTTATTAGAACTCTTTTCTCTGTGAGTTAGCAGACA 3735  
 Qy 2521 AGGGCAATCCCGTTTCTTTTAAAGAGAGAGAGAAACATTCCTAAGAGTAAAGCAAGAT 2580  
 Db 3736 AGGGCAATCCCGTTTCTTTTAAAGAGAGAGAGAAACATTCCTAAGAGTAAAGCAAGAT 3795  
 Qy 2581 TCAAGCCTAGGCTTGTGCACTATATGATTTGTTTTGAAAAATCATTTCAAGGATGTT 2640  
 Db 3796 TCAAGCCTAGGCTTGTGCACTATATGATTTGTTTTGAAAAATCATTTCAAGGATGTT 3855  
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 Db 3856 TACTATCTGATTCAGAAAATGAGACTAGTACCTTTGGTCAAGCTGTAAACAAACCCAT 3915  
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 Qy 3001 AGTCCAGAAAGCTGTGAATTTGAATGAGAAAAAATTAATTTGTTTTTACCACCTT 3060  
 Db 4216 AGTCCAGAAAGCTGTGAATTTGAATGAGAAAAAATTAATTTGTTTTTACCACCTT 4275  
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 Db 4276 CTAACTAAATTTAACTTTTATTCATGCGAATAGACCTTAACCTAAGTGTATA 4335  
 Qy 3121 ACAGTACCTGATTTTGTCACTTACCAATAGAAATCAGACACTTTTACTATATTACA 3180  
 Db 4336 ACAGTACCTGATTTTGTCACTTACCAATAGAAATCAGACACTTTTACTATATTACA 4395  
 Qy 3181 GTTGTGAGATATCGTTGAAGTGAATATTATATCTCAAAACCTAATTGAATTAGACC 3240  
 Db 4396 GTTGTGAGATATCGTTGAAGTGAATATTATATCTCAAAACCTAATTGAATTAGACC 4455  
 Qy 3241 TCTCTGAGATCTTGTTTTAACTATTAACTAATTAACATGTTTAAATTTGATATTGGA 3300  
 Db 4456 TCTCTGAGATCTTGTTTTAACTATTAACTAATTAACATGTTTAAATTTGATATTGGA 4515  
 Qy 3301 TAAATATTTTCAATATATTTGTTCCCTTGTAACTATATTTTATATTTGAAAAACA 3360  
 Db 4516 TAAATATTTTCAATATATTTGTTCCCTTGTAACTATATTTTATATTTGAAAAACA 4575  
 Qy 3361 TCTTTCTGAGAGATTTCCCAAGATTTTCAACAAATGAGTCTTGGCATAACACACAG 3420  
 Db 4576 TCTTTCTGAGAGATTTCCCAAGATTTTCAACAAATGAGTCTTGGCATAACACACAG 4635  
 Qy 3421 AGTAAAGACTGATTTTGAAGGCTTAACATTTGACATTTGGTCTGAGATGCAAGCTGAAAT 3480  
 Db 4636 AGTAAAGACTGATTTTGAAGGCTTAACATTTGACATTTGGTCTGAGATGCAAGCTGAAAT 4695



[illegible]

D	1216	GCTCCAGAGAAAGTCTCCCACTTAGACTTCTGCATCCAGATGTTACAGCCAGAAAGTCT	1275
Q	61	CGTAGGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACTGAGCTCACTGC	120
D	1276	CGTAGGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACTGAGCTCACTGC	1335
Q	121	AACCTTGGCCCTCCAGGTTCAAGAAATTCTCTGTCTCAAGCTCCCGGTAGCTGGAACT	180
D	1336	AACCTTGGCCCTCCAGGTTCAAGAAATTCTCTGTCTCAAGCTCCCGGTAGCTGGAACT	1395
Q	181	ACAGCGCACCCCGGCTAATTTTGTATTGTATGTATGATGGAGTTTCCATATTAAG	240
D	1396	ACAGCGCACCCCGGCTAATTTTGTATTGTATGTATGATGGAGTTTCCATATTAAG	1455
Q	241	CCCGGCTGGTCTTGAACCTCCTGACCTGACGTGATCCACCACTCAAGCTCTTAAAGTG	300
D	1456	CCCGGCTGGTCTTGAACCTCCTGACCTGACGTGATCCACCACTCAAGCTCTTAAAGTG	1515
Q	301	TGGATTACAGGATGAGTACACCCGCCCGGCCAAGGTCATGTTTTAATPAGAAATAC	360
D	1516	TGGATTACAGGATGAGTACACCCGCCCGGCCAAGGTCATGTTTTAATPAGAAATAC	1575
Q	361	TTGAATGGTTACTTAAACCAACAGGAAACAGCAAAAGCTGATATTAATTCAGGGATTC	420
D	1576	TTGAATGGTTACTTAAACCAACAGGAAACAGCAAAAGCTGATATTAATTCAGGGATTC	1635
Q	421	TTGGGATGGGGAATGTGTGACATGAGCTGCTGCTAGTCTCCAGACCACTGGTCTCTACA	480
D	1636	TTGGGATGGGGAATGTGTGACATGAGCTGCTGCTAGTCTCCAGACCACTGGTCTCTACA	1695
Q	481	CTTCTCTCCATCTCATATTTTCAGGCTAAGTATACATTTATTCACATGCTTTGTG	540
D	1696	CTTCTCTCCATCTCATATTTTCAGGCTAAGTATACATTTATTCACATGCTTTGTG	1755
Q	541	GTAAGCCTCCACATGCTTACTGAAATPAGATATACATACTATGTTCCATTGGGGCCA	600
D	1756	GTAAGCCTCCACATGCTTACTGAAATPAGATATACATACTATGTTCCATTGGGGCCA	1815
Q	601	TCTGTGTGTGTATAGGAGGAGGAGGCAATACCCAGAGACTCTTGAAGCCCCGGCAG	660
D	1816	TCTGTGTGTGTATAGGAGGAGGAGGCAATACCCAGAGACTCTTGAAGCCCCGGCAG	1875
Q	661	AGGTTTCTCTCCAGCTGGGGGAGACCTGCAGACCCCGGGGTCTGGGTGTCCTAGCA	720
D	1876	AGGTTTCTCTCCAGCTGGGGGAGACCTGCAGACCCCGGGGTCTGGGTGTCCTAGCA	1935
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Q	901	GTGACAGTTTCTCATGGAAGAGTGCAGAAAGAAATTAATAGCAGCCAACTTAAACCA	960
D	2116	GTGACAGTTTCTCATGGAAGAGTGCAGAAAGAAATTAATAGCAGCCAACTTAAACCA	2175
Q	961	GTGTGAAAAGAAAGGAAATTAACAACATCTTGAAGAAATGTGGGAGCAATCCTTTAACAA	1020
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 Qy 3241 TCCGCTGAGATCTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3300  
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[illegible]

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	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-09-306-828-34	
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Best Local Similarity	99.9%	Pred. No. 0 ;
Matches 4051 ;	Conservative 0 ;	Mismatches 2 ; Indels 4 ; Gaps 3
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QY	121	AACCTCTGCTCCCGAGGTTCAAGCAATCTCTGTCTAAGCTCCCGGTAGCTGGACT 180
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QY	181	ACAGGCGACGCGCCGGCTAATTTTGTATGTTAGTAGAGATGGGGTTCAACATATTAG 240
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RESULT 8  
US-09-056-285A-1

; Sequence No. Application US/09056285A

; Patent No. 6403307

; GENERAL INFORMATION:

; APPLICANT: Stone, Edwin M.

; Sheffield, Val C.

; Alward, Wallace L.M.

; Fingert, John

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; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,285A
; FILING DATE: 07-Apr-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-010.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-056-285A-1

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Query Match      46.2%; Score 2773.4; DB 3; Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

Qy      2216 AGCGAGGAGGAGAGAGAGAGAGAGAGATGATGATGACAGAGAGAGAGATTCAT 2275
Db      1 AGCGAGGAGGAGAGAGAGAGAGAGAGAGATGATGATGACAGAGAGAGAGATTCAT 59

Qy      2276 TCAAGGAGGAGGAGAGAGAGAGAGAGATTAATATCCAGCGATCTGGGTTCTAGAG 2335
Db      60 TCAAGGAGGAGGAGAGAGAGAGAGAGAGATTAATATCCAGCGATCTGGGTTCTAGAG 119

Qy      2336 GCGAGGCTATATTTGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2395
Db      120 GCGAGGCTATATTTGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179

Qy      2396 AATATATATTTTCTTTTCAAGCTGATTAATTTCTGAGCAAGTCAAGAGTATTAATCTG 2455
Db      180 AATATATATTTTCTTTTCAAGCTGATTAATTTCTGAGCAAGTCAAGAGTATTAATCTG 239

Qy      2456 AGGCTGAAGATTAATTAATTTCTTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2515
Db      240 AGGCTGAAGATTAATTAATTTCTTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299

Qy      2516 GCACAGGAGCAATCCCGTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2575
Db      300 GCACAGGAGCAATCCCGTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359

Qy      2576 CAGATTCAAGCTTGAAGTTGCTGCTGATATATGATTTGTTTGAAGAGATTAATTAAT 2635
Db      360 CAGATTCAAGCTTGAAGTTGCTGCTGATATATGATTTGTTTGAAGAGATTAATTAAT 419

Qy      2636 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695
Db      420 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479

Qy      2696 CCATTTGTATATGCTCAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2755
Db      480 CCATTTGTATATGCTCAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539

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[illegible]

Qy	3834	TATTGGGATATGGGTGCATTAATTGGGATGTTCTTTTAAAAAGAACTCCAAACAGACT	3893
Db	1620	TATTGGGATATGGGTGCATTAATTGGGATGTTCTTTTAAAAAGAACTCCAAACAGACT	1679
Qy	3894	TTGGAAGGTTATTTTCTAAGAACTGTGTGGCAGCGTGAAGGCAACCCCTGTGCACA	3953
Db	1680	TTGGAAGGTTATTTTCTAAGAACTGTGTGGCAGCGTGAAGGCAACCCCTGTGCACA	1739
Qy	3954	GCCCCACCAAGCTTCAGGTGGCCACTCTGTCTTCCCATGAAGGGCTGGCTCCCACT	4013
Db	1740	GCCCCACCAAGCTTCAGGTGGCCACTCTGTCTTCCCATGAAGGGCTGGCTCCCACT	1799
Qy	4014	ATAATAAACTCTCTGAGACTCAGGCATGAGCCAGAGGCCAACCCATCCAGGCACCTC	4073
Db	1800	ATAATAAACTCTCTGAGACTCAGGCATGAGCCAGAGGCCAACCCATCCAGGCACCTC	1859
Qy	4074	TCAGACACGACAGGCTTTCAGAGGAAGCCTCACCAAGCCTCTGCATATGAGTTCTTCTG	4133
Db	1860	TCAGACACGACAGGCTTTCAGAGGAAGCCTCACCAAGCCTCTGCATATGAGTTCTTCTG	1919
Qy	4134	TGCAGGTGCTGTCAGCTTTTGAGCCTGAGATGCGAGCTGTCCAGTCTGCTTCTGACCTG	4193
Db	1920	TGCAGGTGCTGTCAGCTTTTGAGCCTGAGATGCGAGCTGTCCAGTCTGCTTCTGACCTG	1979
Qy	4194	CCTGTGTGGGATGTGTGGGGCCAGACACACTCAGCTCAGAAAGGCCAATGACAGAGTGG	4253
Db	1980	CCTGTGTGTGGGATGTGTGGGGCCAGACACACTCAGCTCAGAAAGGCCAATGACAGAGTGG	2039
Qy	4254	CCGATGSCAGTATPACCTTCAGTGTGGCCAGTCCCATATGAAATCCAGCTGCCAGAGCAGAG	4313
Db	2040	CCGATGSCAGTATPACCTTCAGTGTGGCCAGTCCCATATGAAATCCAGCTGCCAGAGCAGAG	2099
Qy	4314	CCAGGCAATGTCACTCATCTAATCTTACAGAGACACAGACACCCAACTTACACT	4373
Db	2100	CCAGGCAATGTCACTCATCTAATCTTACAGAGACACAGACACCCAACTTACACT	2159
Qy	4374	GGAGGCCAACAAAGCTGCACTCAGCTCCCTGAGAGAGCTTCCTCAACCAATTGACCTTGA	4433
Db	2160	GGAGGCCAACAAAGCTGCACTCAGCTCCCTGAGAGAGCTTCCTCAACCAATTGACCTTGA	2219
Qy	4434	CCAGGCTGCAAGGCCCCCAGAGACCCAGAGAGGGGCTGACAGAGGAGCTGGGCACTTGAG	4493
Db	2220	CCAGGCTGCAAGGCCCCCAGAGACCCAGAGAGGGGCTGACAGAGGAGCTGGGCACTTGAG	2279
Qy	4494	GCGGAGCGGGACACAGCTGGAACCCAAACACAGAGTTGAGACTGTCTTACAGCAACT	4553
Db	2280	GCGGAGCGGGACACAGCTGGAACCCAAACACAGAGTTGAGACTGTCTTACAGCAACT	2339
Qy	4554	CCTCCAGACACAGTCAAGTTCTGAGAGAAAGAAAGCAATGAGCGCAAGAAATGAGAA	4613
Db	2340	CCTCCAGACACAGTCAAGTTCTGAGAGAAAGAAAGCAATGAGCGCAAGAAATGAGAA	2399
Qy	4614	TCGTGCCAGAGGTTGGAAAGCAGACGCCAGAGGTAGCAAGGCTGTGAAAGGGGCCAGTG	4673
Db	2400	TCGTGCCAGAGGTTGGAAAGCAGACGCCAGAGGTAGCAAGGCTGTGAAAGGGGCCAGTG	2459
Qy	4674	TCCCCAGACCAGACACACTGCTCGGGCTGTGCCACACAGGCTCCAGAGAGGTAAGATGC	4733
Db	2460	TCCCCAGACCAGACACACTGCTCGGGCTGTGCCACACAGGCTCCAGAGAGGTAAGATGC	2519
Qy	4734	AGAGTGGGGGAGACTCTGAGTTCAGACAGTGAATATGGCTTCGTAAGTGAACCTGTACAGGGGC	4793
Db	2520	AGAGTGGGGGAGACTCTGAGTTCAGACAGTGAATATGGCTTCGTAAGTGAACCTGTGTACAGGGGC	2579
Qy	4794	TTCCAGGCTCCCTGCGCTGCCCTTCTCTCTAGAGCTGACAGAGCTAGCACAAGACAGATGA	4853
Db	2580	TTCCAGGCTCCCTGCGCTGCCCTTCTCTCTAGAGCTGACAGAGCTAGCACAAGACAGATGA	2639
Qy	4854	ATTAAAGAAAGCAGACGATCACCTTCAAGTATTAATAATTAATTAAGTCTCTGAGAGCTT	4913
Db	2640	ATTAAAGAAAGCAGACGATCACCTTCAAGTATTAATAATTAATTAAGTCTCTGAGAGCTT	2699
Qy	4914	CATTYAGATTAGTGGTTCAGAGTCTTGTGCCCCCTCCATGTCACTTTTCAAGTCCATATAG	4973

Db 2700 CATTGATTAGTGGTTCAGAGTCTTGCCCTCCATGTCAGTTTTCAGTCCATAG 2759  
QY 4974 CAAAAGAGAAATAAAGACCGGGTGAATGTGTCCGAT 5014  
Db 2760 CAAAAGAGAAATAAAGACCGGGTGAATGTGTCCGAT 2800

RESULT 9  
US-10-017-870-10  
; Sequence 10, Application US/10017870  
; Patent No. 6727354  
; GENERAL INFORMATION:  
; APPLICANT: HUMANG, DOUG HUI  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS  
; FILE REFERENCE: 034827-1401  
; CURRENT APPLICATION NUMBER: US/10/017, 870  
; CURRENT FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 2800  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-017-870-10

Query Match 46.2%; Score 2773.4; DB 3; Length 2800;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 2216 AGCGCAGGAGAGAGAGAGAGAGAGAGATAGTATAGCAAGAGAGAGAGATTCAT 2275  
Db 1 AGCGCAGGAGAGAGAGAG-AAAAGAGAGAGATAGTATAGCAAGAGAGAGATTCAT 59  
QY 2276 TCAGGCGCTGTGGAAATTGACACAGAGATTTATGTCACGTGATCTGAGTTCTAGAG 2335  
Db 60 TCAGGCGCTGTGGAAATTGACACAGAGATTTATGTCACGTGATCTGAGTTCTAGAG 119  
QY 2336 GCAGGCGCTATATTGTGGGGGAGAGAGAGAGATTCAGAGAGCGGAGAGACCTGATTTCT 2395  
Db 120 GCAGGCGCTATATTGTGGGGGAGAGAGAGAGATTCAGAGAGCGGAGAGACCTGATTTCT 179  
QY 2396 AATACTATATTTTCTCTTTCACAGCTGAGTAATTTCTGACCAAGTCAAGTAGTACTG 2455  
Db 180 AATACTATATTTTCTCTTTCACAGCTGAGTAATTTCTGACCAAGTCAAGTAGTACTG 239  
QY 2456 AGGCTGTAGATTACTTACTGTTCTCTTATAGAACTCTTTTCTCTGTGAGTTAGCA 2515  
Db 240 AGGCTGTAGATTACTTACTGTTCTCTTATAGAACTCTTTTCTCTGTGAGTTAGCA 299  
QY 2516 GCAAGAGGCGAATCCCGTTCTTTTACAGAGAGAGAGAGATTCCTAAGAGTAAGCCAA 2575  
Db 300 GCAAGAGGCGAATCCCGTTCTTTTACAGAGAGAGAGAGATTCCTAAGAGTAAGCCAA 359  
QY 2576 CAGATTCAAGCTGAGTCTTGCTGACTATATGTTGGTTTGTGAAAAATCATTTACAGG 2635  
Db 360 CAGATTCAAGCTGAGTCTTGCTGACTATATGTTGGTTTGTGAAAAATCATTTACAGG 419  
QY 2636 ATGTTTACTATCTGATTGAGAAATGAGACTAGACCTTGGTCACTGTAAACAAACA 2695  
Db 420 ATGTTTACTATCTGATTGAGAAATGAGACTAGACCTTGGTCACTGTAAACAAACA 479  
QY 2696 CCCATTGTAATGCTCAAGTTCAGGCTTAATCTGAGAACCAATCAATTAAGATAGAA 2755  
Db 480 CCCATTGTAATGCTCAAGTTCAGGCTTAATCTGAGAACCAATCAATTAAGATAGAA 539  
QY 2756 TCTTTAGAGCAAACTGTGTTCTCCACTCTGAGAGTGAAGTCTGCAAGGCAATTTGAAA 2815  
Db 540 TCTTTAGAGCAAACTGTGTTCTCCACTCTGAGAGTGAAGTCTGCAAGGCAATTTGAAA 599  
QY 2816 TATTTACTTCAAGATTTGACATGTTGTGGTATTAACAATPAAAGTTCTCAAG 2875  
Db 600 TATTTACTTCAAGATTTGACATGTTGTGGTATTAACAATPAAAGTTCTCAAG 659

QY 2876 CAATCATATTTCAAGTGGCTTAAAGTATCTTCTGACAGTTTGGTATTTATGGCTTA 2935  
Db 660 CAATCATATTTCAAGTGGCTTAAAGTATCTTCTGACAGTTTGGTATTTATGGCTTA 719  
QY 2936 TTGCCATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGAAAGCAGGATTTAA 2995  
Db 720 TTGCCATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGAAAGCAGGATTTAA 779  
QY 2996 CCTACAGTCCAGAAAGCTGTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3055  
Db 780 CCTACAGTCCAGAAAGCTGTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 839  
QY 3056 ACCCTCTAATCTAAATTTAACTTTATTCATTTGGGATAGAGCCATAACTCAAGTGG 3115  
Db 840 ACCCTCTAATCTAAATTTAACTTTATTCATTTGGGATAGAGCCATAACTCAAGTGG 899  
QY 3116 TAATAACAGTACCTGTGATTTTGTCAATTAACAATGAAATGACAGATTTATACTATA 3175  
Db 900 TAATAACAGTACCTGTGATTTTGTCAATTAACAATGAAATGACAGATTTATACTATA 959  
QY 3176 TTACAGTTGTTCAGATACGTTGTAAGTGAATTTATTAATTAATTAATTAATTAAT 3235  
Db 960 TTACAGTTGTTCAGATACGTTGTAAGTGAATTTATTAATTAATTAATTAATTAATTA 1019  
QY 3236 AGACCTCCCTGCTGATCTTGTGTTTAACTATTAATAAATCTGTTAAATTTGATAT 3295  
Db 1020 AGACCTCCCTGCTGATCTTGTGTTTAACTATTAATAAATCTGTTAAATTTGATAT 1079  
QY 3296 TTTGATTAATCATATTTTCAATTTATCATTTGTTTCTTGTATCTATATTTATTAATTA 3355  
Db 1080 TTTGATTAATCATATTTTCAATTTATCATTTGTTTCTTGTATCTATATTTATTAATTA 1139  
QY 3356 AAAATCTTTCTGAGAGAGTCCCAATTTCAACAAATGAGTTCTTGGACAGACA 3415  
Db 1140 AAAATCTTTCTGAGAGAGTCCCAATTTCAACAAATGAGTTCTTGGACAGACA 1199  
QY 3416 CACAGAGTAAGAACTGATTTAGAGCTTAACTTGAATTTGGTCTGAGATGCAAGCTG 3475  
Db 1200 CACAGAGTAAGAACTGATTTAGAGCTTAACTTGAATTTGGTCTGAGATGCAAGCTG 1259  
QY 3476 AAATTAAGAAAGTTCTCCCAAGATPACAGTTGTTTAAAGCTAGAGGAGAGAGAGAA 3535  
Db 1260 AAATTAAGAAAGTTCTCCCAAGATPACAGTTGTTTAAAGCTAGAGGAGAGAGAGAA 1319  
QY 3536 TCTGCCGCTTATAGAAATGCTCTCCCTGAGAGCTGTGAGAGGCTGCTCTGTGTTCT 3595  
Db 1320 TCTGCCGCTTATAGAAATGCTCTCCCTGAGAGCTGTGAGAGGCTGCTCTGTGTTCT 1379  
QY 3596 GAGCTGGCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3655  
Db 1380 GAGCTGGCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439  
QY 3656 TTCTGAGATGAGTGGCTGGGACAGTGCAGTTCATGAGATTTGCAAGAGTAAAGTAA 3715  
Db 1440 TTCTGAGATGAGTGGCTGGGACAGTGCAGTTCATGAGATTTGCAAGAGTAAAGTAA 1499  
QY 3716 TATAAATAGAAATATATCTTGTGAAATGAGACACACAGTAGTCTGTGTAAGTGTG 3775  
Db 1500 TATAAATAGAAATATATCTTGTGAAATGAGACACACAGTAGTCTGTGTAAGTGTG 1559  
QY 3776 TGTAC-GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3833  
Db 1560 TGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1619  
QY 3834 TATTTGGGATGAGGAGCAATAATTTGGAGTGTCTTTTAAAGAAAGAACTCCAAACAGCT 3893  
Db 1620 TATTTGGGATGAGGAGCAATAATTTGGAGTGTCTTTTAAAGAAAGAACTCCAAACAGCT 1679  
QY 3894 TCTGGAAGTATATTTTCTAAGAAATCTTGTGAGAGCTGGAAGGCAACCCCTGTGACA 3953  
Db 1680 TCTGGAAGTATATTTTCTAAGAAATCTTGTGAGAGCTGGAAGGCAACCCCTGTGACA 1739



QY	2756	TCCTTAGAGCAAACTGTGTTCTCCACTGAGGTGAGTCTGGCAGGGCAGTTGGAAA	2815
Db	540	TCCTTAGAGCAAACTGTGTTCTCCACTGAGGTGAGTCTGGCAGGGCAGTTGGAAA	599
QY	2816	TATTTACTTCAAGATATTGACACTGTGTGGTATTAAACAATAAAGTTGCTCAAGG	2875
Db	600	TATTTACTTCAAGATATTGACACTGTGTGGTATTAAACAATAAAGTTGCTCAAGG	659
QY	2876	CAATCATTTATTTAAGGGCTTAAAGTTACTTCTGACAGTTTGGTATTTATTTGGCTA	2935
Db	660	CAATCATTTATTTAAGGGCTTAAAGTTACTTCTGACAGTTTGGTATTTATTTGGCTA	719
QY	2936	TTGCAATTTGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATTA	2995
Db	720	TTGCAATTTGCTTTTGTGTTTCTCTTTGGGTTTATTAATGTAAGCAGGATTTATTA	779
QY	2996	CTTACAGTCCAGAAAGCTGTGAAATTTGAAATGAGAAAAAATTAATTTTGTATACC	3055
Db	780	CTTACAGTCCAGAAAGCTGTGAAATTTGAAATGAGAAAAAATTAATTTTGTATACC	839
QY	3056	ACCTTCACTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA	3115
Db	840	ACCTTCACTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA	899
QY	3116	TAAATAACAGTACCTGTGATTTTGTCAATTACCAATAGAAATCAGACATTTTACTATA	3175
Db	900	TAAATAACAGTACCTGTGATTTTGTCAATTACCAATAGAAATCAGACATTTTACTATA	959
QY	3176	TTTACAGTTGTGCAAGATACCTGTGAAAGTAAATTTATTAATCTAAACATACTTTGAAT	3235
Db	960	TTTACAGTTGTGCAAGATACCTGTGAAAGTAAATTTATTAATCTAAACATACTTTGAAT	1019
QY	3236	AGACCTCCGCTGAGTCTGTGTTTAAACATTAATTAACATGTTTAAATTTGATAT	3295
Db	1020	AGACCTCCGCTGAGTCTGTGTTTAAACATTAATTAACATGTTTAAATTTGATAT	1079
QY	3296	TTTGTATATCATATTTCAATTATCATTTGTTTCTTTGTAAATCTATAATTTATTAATTTGA	3355
Db	1080	TTTGTATATCATATTTCAATTATCATTTGTTTCTTTGTAAATCTATAATTTATTAATTTGA	1139
QY	3356	AAAACATCTTTCTGAGAAAGTCCCAAGATTTCAACATGAGGTTCTTGGCATGACACA	3415
Db	1140	AAAACATCTTTCTGAGAAAGTCCCAAGATTTCAACATGAGGTTCTTGGCATGACACA	1199
QY	3416	CACAGATAGAACTGATTTAGAGGCTAACATTGACATTGTGCTGAGATGCAAACTG	3475
Db	1200	CACAGATAGAACTGATTTAGAGGCTAACATTGACATTGTGCTGAGATGCAAACTG	1259
QY	3476	AAATTAGAAAGTTCTCCCAAGATACAGATTGTTTAAAGCTAGAGGGTGAAGGGGGAAA	3535
Db	1260	AAATTAGAAAGTTCTCCCAAGATACAGATTGTTTAAAGCTAGAGGGTGAAGGGGGAAA	1319
QY	3536	TCGCGCGCTTCTATAGAAATGCTCTCCCTGAGACCTGTAGGGTGTCTCTTGTGTTCT	3595
Db	1320	TCGCGCGCTTCTATAGAAATGCTCTCCCTGAGACCTGTAGGGTGTCTCTTGTGTTCT	1379
QY	3596	GGCTGCTGTATATTTTCTCTGTCCTGCTGCTAAGCTTTAAAGCACTTGTGATCTCCAG	3655
Db	1380	GGCTGCTGTATATTTTCTCTGTCCTGCTGCTAAGCTTTAAAGCACTTGTGATCTCCAG	1439
QY	3656	TTCTAGCATAGTCTGAGCAAGTGCAGAGTCTCAATAGATTGACAGTGAATGGAAA	3715
Db	1440	TTCTAGCATAGTCTGAGCAAGTGCAGAGTCTCAATAGATTGACAGTGAATGGAAA	1499
QY	3716	TATTAACATAGAAATATATCTTGTGTAATCAGACACCAAGTATGCTGTGTATAGTGTG	3775
Db	1500	TATTAACATAGAAATATATCTTGTGTAATCAGACACCAAGTATGCTGTGTATAGTGTG	1559
QY	3776	TGTATC--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3833
Db	1560	TGTATC--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1619

QY	3834	TATTTGGGATATGAGGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGCT	3893
Db	1620	TATTTGGGATATGAGGTGATTAATTTGGATGTTCTTTTAAAGAACTCCAAACAGCT	1679
QY	3894	TCTGAAGGTTATTTTCTAAGAACTTGTCTGACAGGTGAAGCAACCCCTGTGTGACA	3953
Db	1680	TCTGAAGGTTATTTTCTAAGAACTTGTCTGACAGGTGAAGCAACCCCTGTGTGACA	1739
QY	3954	GCCCAACCCAGCTCACTGTGCTCACTGTCTTCCCCCAATGAAGGCTGTGCCAGT	4013
Db	1740	GCCCAACCCAGCTCACTGTGCTCACTGTCTTCCCCCAATGAAGGCTGTGCCAGT	1799
QY	4014	ATATATTAACCTCTCTGAGAGCTCAGGCATGAGCCAGCAAGGCCCATTCAGGCACTC	4073
Db	1800	ATATATTAACCTCTCTGAGAGCTCAGGCATGAGCCAGCAAGGCCCATTCAGGCACTC	1859
QY	4074	TCAGCACAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCATAGAGTTCTTCTG	4133
Db	1860	TCAGCACAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCATAGAGTTCTTCTG	1919
QY	4134	TGCACGTTGCTGACGTTTGGGCTGTGAAATGCCAGCTTTCACGCTGCTGTGGCTTG	4193
Db	1920	TGCACGTTGCTGACGTTTGGGCTGTGAAATGCCAGCTTTCACGCTGCTGTGGCTTG	1979
QY	4194	CTGTGTGTGGAATGTGGGGGCCAGGACAGTCAAGTCAAGAAAGCCAAATGACAGATGG	4253
Db	1980	CTGTGTGTGGAATGTGGGGGCCAGGACAGTCAAGTCAAGAAAGCCAAATGACAGATGG	2039
QY	4254	CCGATGCCAGTATACCTTCAAGTGTGGCCAGTCCCAATGAATCAGCTGCCAGAGCAGAG	4313
Db	2040	CCGATGCCAGTATACCTTCAAGTGTGGCCAGTCCCAATGAATCAGCTGCCAGAGCAGAG	2099
QY	4314	CCAGGCCATGTGATGTCATCTAATTAACAGAGACAGCAGACCCAAAGCTTTAGACCT	4373
Db	2100	CCAGGCCATGTGATGTCATCTAATTAACAGAGACAGCAGACCCAAAGCTTTAGACCT	2159
QY	4374	GGAGGCCACCAAAAGCTCGACTAGCTCCCTGAGAGGCTCTCCCAATTTGACCTTTGGA	4433
Db	2160	GGAGGCCACCAAAAGCTCGACTAGCTCCCTGAGAGGCTCTCTCCCAATTTGACCTTTGGA	2219
QY	4434	CCAGGCTGACAGGCCCCAGAGAACCCAGAGGGGCTGACAGAGGAGCTGTGGACCTGAG	4493
Db	2220	CCAGGCTGACAGGCCCCAGAGAACCCAGAGGGGCTGACAGAGGAGCTGTGGACCTGAG	2279
QY	4494	GGGGAGCGGGACCAAGCTGGAACCCAAACAGAGATTTGAGACTGCTTACAGCAACT	4553
Db	2280	GGGGAGCGGGACCAAGCTGGAACCCAAACAGAGATTTGAGACTGCTTACAGCAACT	2339
QY	4554	CCTCGGAGCAAGTCAATTTCTGAGAGAGAGAAAGGACCTTAAGGCAGAAATGAGAA	4613
Db	2340	CCTCGGAGCAAGTCAATTTCTGAGAGAGAGAAAGGACCTTAAGGCAGAAATGAGAA	2399
QY	4614	TCTGCGCAGAGGTTGGAAGAGCAGCAGGAGGTAGCAAGGCTGAGAAAGGGGCAAGT	4673
Db	2400	TCTGCGCAGAGGTTGGAAGAGCAGCAGGAGGTAGCAAGGCTGAGAAAGGGGCAAGT	2459
QY	4674	TTCCCAAGACCGGAGCACTGCTCGGGCTGTGTCCACCAAGCTTCCAGAGAAAGTAAATGC	4733
Db	2460	TTCCCAAGACCGGAGCACTGCTCGGGCTGTGTCCACCAAGCTTCCAGAGAAAGTAAATGC	2519
QY	4734	AGAGTGGGGGGGCTCTGAGTTTCAAGAGGTGATATGCTCTGTAGTAACTTGTCAAGGGC	4793
Db	2520	AGAGTGGGGGGGCTCTGAGTTTCAAGAGGTGATATGCTCTGTAGTAACTTGTCAAGGGC	2579
QY	4794	TTCAGGCTCTCCCTGCTGCTCCCTTCTCTTCAAGAGCTGACAGCTGACAAAGACATGA	4853
Db	2580	TTCAGGCTCTCCCTGCTGCTCCCTTCTCTTCAAGAGCTGACAGCTGACAAAGACATGA	2639
QY	4854	ATTTAAGGAAGCAGCAGCATCACTTCAAGTATTAATTAATTTAGTCTTCTGAGAGCTT	4913
Db	2640	ATTTAAGGAAGCAGCAGCATCACTTCAAGTATTAATTAATTTAGTCTTCTGAGAGCTT	2699
QY	4914	CATTTAGATTAATGTTTCAAGATTTCTGTGCCCTCCATGTCAAGTTTCAAGTCCATAG	4973

Db 2700 CATTAGATTAGTGGTTGAGGTTCTGTGCCCCCTCCATGTCAGTTTTCAGAGTCCATAG 2759  
QY 4974 CAAAAGGAAATATAAGACCGGTGAGTGTCTGCAT 5014  
Db 2760 CAAAAGGAAATATAAGACCGGTGAGTGTCTGCAT 2800

RESULT 11  
US-08-822-999-1  
Sequence 1, Application US/08822999  
Patent No. 6271026  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
TITLE OF INVENTION: GLAUCOMA COMPOSITIONS AND THERAPEUTIC  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HONG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,999  
FILING DATE: 21-MAR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/791,347  
FILING DATE: 30-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/748,479  
FILING DATE: 08-NOV-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/234,218  
FILING DATE: 28-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.27  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2166 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-822-999-1

Query Match 12.8%; Score 770; DB 3; Length 2166;  
Best local similarity 98.3%; Pred. No. 3.6e-178;  
Matches 773; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3940 CCCCCCTGTGACAGGCCCAACCCAGCTCACTGCGCACCTGTGTTTCCCCCATGAAG 3999  
Db 1 CCCCCCTGTGACAGGCCCAACCCAGCTCACTGCGCACCTGTGTTTCCCCCATGAAG 60  
QY 4000 GCTGGCTCCCGCATATATATAAACCCTCTGAGAGCTCAGGACATGAGCCGCAAGGCGACC 4059  
Db 61 GCTGGCTCCCGCATATATATAAACCCTCTGAGAGCTCAGGACATGAGCCGCAAGGCGACC 120  
QY 4060 CATCCAGGACCTCTCAGCAGACAGAGCTTTCAGAGGAAGCCTCACCAAGCCTCTGCA 4119

Db 121 CATTAGGACCTTTGAGCAGACAGAGAGCTTCCAGAGGAAGCTTCAACAGCTCTGCA 180  
QY 4120 ATAGAGTTCTTCTGTGACAGTGTGAGCTTTGGGCTGAGATGACAGCTGTCCAGCTG 4179  
Db 181 ATAGAGTTCTTCTGTGACAGTGTGAGCTTTGGGCTGAGATGACAGCTGTCCAGCTG 240  
QY 4180 CTGCTTCTGCGCTGCTGTGTGTGGATGTGGGGCCAGAGACAGCTCAGAGGAAGGCC 4239  
Db 241 CTGCTTCTGCGCTGCTGTGTGTGGATGTGGGGCCAGAGACAGCTCAGAGGAAGGCC 300  
QY 4240 AATGACAGAGTGGCCCATGTCAGTATACCTTCACTGTGTGCTCCCATGAAATCCAGC 4299  
Db 301 AATGACAGAGTGGCCCATGTCAGTATACCTTCACTGTGTGCTCCCATGAAATCCAGC 360  
QY 4300 TGCCCAAGCAGACCCAGGCGCATGTCACTATCATTAATTACAGAGAGCAGAGCACC 4359  
Db 361 TGCCCAAGCAGACCCAGGCGCATGTCACTATCATTAATTACAGAGAGCAGAGCACC 420  
QY 4360 CAACGCTTAGACTGTGAGGCGCACCAAGAGTCTGACTCAGCTCCCTGAGAGGCTCTCCAC 4419  
Db 421 CAACGCTTAGACTGTGAGGCGCACCAAGAGTCTGACTCAGCTCCCTGAGAGGCTCTCCAC 480  
QY 4420 CAATTGACCTTGAACAGAGCTGCGAGGCCCAAGAGACCCAGAGAGGCTGCAAGAGAG 4479  
Db 481 CAATTGACCTTGAACAGAGCTGCGAGGCCCAAGAGACCCAGAGAGGCTGCAAGAGAG 540  
QY 4480 CTGGGCAACCCGAGGCGGAGACCGGAGACAGCTGGAACCCAAACAGAGAGTTGAGACT 4539  
Db 541 CTGGGCAACCCGAGGCGGAGACCGGAGACAGCTGGAACCCAAACAGAGAGTTGAGACT 600  
QY 4540 GCTTACAGCAACTCTCTCCGAGAGACAGTCACTTCTGAGGAAGAGAGAGCGACTAAG 4599  
Db 601 GCTTACAGCAACTCTCTCCGAGAGACAGTCACTTCTGAGGAAGAGAGAGCGACTAAG 660  
QY 4600 CAAGAAATGGAATCTGGCCAGAGGTTGGAAGACAGACCCAGAGAGTACAGAGCTG 4659  
Db 661 CAAGAAATGGAATCTGGCCAGAGGTTGGAAGACAGACCCAGAGAGTACAGAGCTG 720  
QY 4660 AGAAGGGGCGAGTGTCCAGACCGAGAGCACTGCTGGGGGTGTGCCACAGGCTCCAGA 4719  
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QY 4720 GAAGGT 4725  
Db 781 GAAGTT 786

RESULT 12  
US-08-938-669A-26  
Sequence 26, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thad D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A



FILED DATE: 435  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1548 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-938-669A-26

Query Match 10.7%; Score 640.4; DB 3; Length 1548;  
Best Local Similarity 99.8%; Pred. No. 1.6e-146;  
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4084 AGAGCTTTCCAGAGAGAGCTTCAAGAGCTTGCATGAGTTCTTCTGTGACGTTGC 4143  
DB 1 AGAGCTTTCCAGAGAGAGCTTCAAGAGCTTGCATGAGTTCTTCTGTGACGTTGC 60  
QY 4144 TGCAGCTTTGGGCTTGAAGATGCGAGCTGTCAGCTGTGCTTGTGCTGCTGCTGTG 4203  
DB 61 TGCAGCTTTGGGCTTGAAGATGCGAGCTGTCAGCTGTGCTTGTGCTGCTGCTGTG 120  
QY 4204 GATGTGGGGCCAGAGACAGCTCAAGCTCAAGAGGCCAATGACAGAGTGGCCGATGCG 4263  
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DB 601 CGAGACACTGCTCGGGCTGTGCGACAGAGCTTCCAGAGAGAGT 642

RESULT 13  
US-09-306-828-26

Sequence 26, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And  
CURRENT APPLICATION NUMBER: US/09/306,828  
EARLIER APPLICATION NUMBER: US 09/227,881  
EARLIER FILING DATE: 1999-05-07  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 26  
LENGTH: 1548  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-26

Query Match 10.7%; Score 640.4; DB 3; Length 1548;  
Best Local Similarity 99.8%; Pred. No. 1.6e-146;  
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4084 AGAGCTTTCCAGAGAGAGCTTCAAGAGCTTGCATGAGTTCTTCTGTGACGTTGC 4143  
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DB 301 AAAGCTCGACTCAGCTCCCTGGAAGAGCTCTTCCACCAATTGACCTTGAAGCAAGCTGCC 360  
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DB 361 AGGCCCCAGAGAGCCAGAGAGGGGCTGCAAGAGGAGCTGGGCACTTGAAGGCGGAGCGG 420  
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DB 601 CGAGACACTGCTCGGGCTGTGCGACAGAGCTTCCAGAGAGAGT 642

RESULT 14  
US-08-645-900A-2  
Sequence 2, Application US/08645900A  
Patent No. 5849879





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GenCore version 5.1.7  
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OM nucleic - nucleic search, using SW model

Run on: March 24, 2006, 02:05:33 ; Search time 4277 Seconds  
(without alignments)  
11600.717 Million cell updates/sec

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Perfect score: 6000  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:  
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10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5998.4	99.9	6000	US-10-509-595-1	Sequence 1, Appl
2	5976.8	99.6	37252	US-10-087-192-1228	Sequence 1228, Ap
3	4888.8	81.5	6169	US-10-244-633-3	Sequence 3, Appl
4	4069.4	67.8	5300	US-09-985-637A-1	Sequence 1, Appl
5	4069.4	67.8	5300	US-10-244-633-1	Sequence 1, Appl
6	4069.4	67.8	5300	US-10-741-339-1	Sequence 1, Appl
7	4057.4	67.6	5304	US-10-244-633-2	Sequence 2, Appl
8	4015.8	66.9	5271	US-10-244-633-3	Sequence 3, Appl
9	2773.4	46.2	2800	US-09-952-464A-1	Sequence 1, Appl
10	2773.4	46.2	2800	US-10-017-870-10	Sequence 10, Appl
11	2773.4	46.2	2800	US-10-278-698-294	Sequence 294, App
12	2773.4	46.2	2800	US-10-278-698-808	Sequence 808, App
13	2773.4	46.2	2800	US-10-803-557-10	Sequence 10, Appl
14	2773.4	46.2	2800	US-10-956-243-1	Sequence 1, Appl
15	1068.8	17.8	1086	US-10-240-425-1586	Sequence 1586, Ap
16	1068.8	17.8	1086	US-10-723-860-927	Sequence 927, App
17	1068.8	17.8	1086	US-10-756-149-932	Sequence 932, App
18	668.4	11.1	2082	US-10-087-192-1229	Sequence 1229, Ap
19	668.4	11.1	2115	US-10-723-860-5503	Sequence 5503, Ap
20	640.4	10.7	1548	US-10-244-633-26	Sequence 26, Appl
21	631.6	10.5	632	US-09-925-065A-905501	Sequence 905501,
22	629.6	10.5	630	US-09-925-065A-917000	Sequence 917000,
23	626.4	10.4	2061	US-09-844-653-172	Sequence 172, App

24	618	10.3	30057	US-10-087-192-1225	Sequence 1225, Ap
25	608	10.1	2800	US-09-952-464A-4	Sequence 4, Appl
26	608	10.1	2800	US-10-956-243-4	Sequence 4, Appl
27	604.4	10.1	1515	US-09-952-464A-7	Sequence 7, Appl
28	604.4	10.1	1515	US-10-956-243-7	Sequence 7, Appl
29	604.4	10.1	1515	US-10-029-385-25144	Sequence 25144, A
30	570.6	9.5	571	US-09-925-065A-346049	Sequence 346049,
31	543	9.0	545	US-09-925-065A-346051	Sequence 346051,
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33	516.4	8.6	518	US-10-029-385-11435	Sequence 11435, A
34	412	6.9	1991	US-10-108-260A-1807	Sequence 1807, Ap
35	382.8	6.4	1473	US-09-952-464A-9	Sequence 9, Appl
36	382.8	6.4	1473	US-10-956-243-9	Sequence 9, Appl
37	382.8	6.4	1475	US-10-087-192-1226	Sequence 1226, Ap
38	296	4.9	296	US-10-674-124A-1442	Sequence 1442, Ap
39	296	4.9	296	US-10-674-124A-1443	Sequence 1443, Ap
40	281.4	4.7	283	US-10-244-633-37	Sequence 37, Appl
41	225.4	3.8	227	US-10-244-633-38	Sequence 38, Appl
42	194.6	3.2	33744	US-10-388-838-58	Sequence 58, Appl
43	189.8	3.2	37443	US-10-719-993-6853	Sequence 6853, Ap
44	186	3.1	186	US-10-674-124A-1441	Sequence 1441, Ap
45	185.4	3.1	86361	US-10-741-601-5702	Sequence 5702, Ap

ALIGNMENTS

RESULT 1  
US-10-509-595-1  
; Sequence 1, Application US/10509595  
; Publication No. US20050170353A1  
; GENERAL INFORMATION:  
; APPLICANT: Symex Corporation  
; APPLICANT: ASANO, Kaoru  
; APPLICANT: TAKAHARA, Takayuki  
; APPLICANT: NUMADA, Shigehiro  
; APPLICANT: MASAGO, Akimori  
; APPLICANT: KOUCHI, Yasuhiko  
; TITLE OF INVENTION: GENE EXAMINATION METHOD FOR JUDGING THE ONSET RISK OF GLAUCOMA  
; FILE REFERENCE: 083447  
; CURRENT APPLICATION NUMBER: US/10/509,595  
; CURRENT FILING DATE: 2004-09-29  
; PRIOR APPLICATION NUMBER: JP 2002-093443  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: PCT/JP03/03307  
; PRIOR FILING DATE: 2003-03-19  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 6000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-509-595-1  
Query Match 99.9%; Score 5998.4; DB 9; Length 6000;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 1 GCTCCACGAGAGTGTCCCACTGACACTGTGATGCTTACACCTGAGCTCACTGC 60  
QY 61 CGTGAAGGTGAGGCTGTGTCTTACACCTGATGCTTACACCTGAGCTCACTGC 120  
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QY 121 AACCTGCTCCCTCCAGGTTCAAGCAATCTCTGCTCAGCTCCGCTGAGCTGGAGCT 180  
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 Db 241 CCCGGCTGCTTGAACCTCTGACCTCAGTGATCCACCACCTCAGGCTCTTAAAGTC 300  
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 Db 2281 GGCAGTGGGAATTTGACCAAGGATATATGTCACAGTATCTTGGTCTTGAAGGAGGAG 2340  
 Oy 2341 GCTAATTTGTGGGGGAAAAATCAGTTCAAGGAAAGTGGGAGACCTGATTTCTAATAC 2400  
 Db 2341 GCTAATTTGTGGGGGAAAAATCAGTTCAAGGAAAGTGGGAGACCTGATTTCTAATAC 2400  
 Oy 2401 TATATTTTCTTTACAGACTGAGTAATTTGAGCAAGTCAAGGTAAGTAAGTGAAGCT 2460





QY 361 TTGATGCTTTACTAAACCAAGGAAACAGCAAAAGCTGTGATAATTTCAAGGATTC 420  
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Db 6306 TTGATGCTTTACTAAACCAAGGAAACAGCAAAAGCTGTGATAATTTCAAGGATTC 6365  
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QY 421 TTGGGATGGGGAATGGTGGCAATGAGCTGCTGCTTAATCCAGACCACTGGTCTTCATCA 480  
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Db 6366 TTGGGATGGGGAATGGTGGCAATGAGCTGCTGCTTAATCCAGACCACTGGTCTTCATCA 6425  
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QY 481 CTTTCTTCCCTCAATCTCATTTTCAAGGCTAAGTTACATTTTATTCACANAGCTTTTGTG 540  
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Db 6426 CTTTCTTCCCTCAATCTCATTTTCAAGGCTAAGTTACATTTTATTCACANAGCTTTTGTG 6485  
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QY 541 GTAAGCTTCACATCGTTACTGAATAAGATATACATAAATACTAGTTCAATTTGGGSCCA 600  
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Db 6486 GTAAGCTTCACATCGTTACTGAATAAGATATACATAAATACTAGTTCAATTTGGGSCCA 6545  
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QY 601 TCTGTGTGTGTATAGAGGAGAGAGGCAATCCCAAGACTCCTTGAAGCCCCGGCAG 660  
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Db 6546 TCTGTGTGTGTATAGAGGAGAGAGGCAATCCCAAGACTCCTTGAAGCCCCGGCAG 6605  
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QY 661 AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGGACCCGGGGTCTGGGGTCTGAGCA 720  
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Db 6606 AGGTTTCTCTCCAGCTGGGGGAGCCCTGCAAGGACCCGGGGTCTGGGGTCTGAGCA 6665  
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QY 721 ACCTGCAGCCCGTGCACATGATTTTGTATCACTCTCTAGGGACTGTGTCTTCT 780  
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Db 6666 ACCTGCAGCCCGTGCACATGATTTTGTATCACTCTCTAGGGACTGTGTCTTCT 6725  
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QY 781 ATTTCTGTGTGATCTCGTTCAATTCAGGCAATTCATTGACAAATTTATAGATTTATA 840  
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Db 6726 ATTTCTGTGTGATCTCGTTCAATTCAGGCAATTCATTGACAAATTTATAGATTTATA 6785  
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QY 841 TCTGCAGACACCAAGAGCAAAATGTGAGCAAAAGCAATGACCTTACTCTGTGAG 900  
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Db 6786 TCTGCAGACACCAAGAGCAAAATGTGAGCAAAAGCAATGACCTTACTCTGTGAG 6845  
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QY 901 GTGACAGTTTCTCATGGAAGACGTGCAAGAAATTAATAGCAGCACTTAAACCA 960  
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Db 6846 GTGACAGTTTCTCATGGAAGACGTGCAAGAAATTAATAGCAGCACTTAAACCA 6905  
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QY 961 GTGCTGAAAGAAAGAAATTAACACATCTTGAAGATGTGGCAGCATCCCTTAAACA 1020  
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Db 7026 CTTTCAAGCTCTCTCTCATCATGATCAAGCGCTGAGCTGCGCTGCTTCCCTG 7085  
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Db 8166 AAGGGAGAGAAAGAAAGAGAGAGTATAGCAAGAAAGACAGATTCAATCAAG 8225  
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QY 2341 GCTAATTTGTGGGGGAGAAATCAAGTTCAAGGGAGTGGGAGACTGATTTCTAATAC 2400  
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Db 8286 GCTAATTTGTGGGGGAGAAATCAAGTTCAAGGGAGTGGGAGACTGATTTCTAATAC 8345  
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QY 2401 TATATTTTCTTTTCAAGCTGAAGTAATCTGAGCAAGTCAAGAGTGAATGAGGCT 2460  
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Db 8406 GTAAGATTAATTAAGTTTCTCTTATAGAACTTTTCTCTGTGAGTTAGCAGCA 8465  
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Qy 2581 TCAAGCCGAGCTCTTGTGACATATATGATGTTTGTGAAAAATCATTTTCAGGAGTT 2640  
Db 8526 TCAAGCCGAGCTCTTGTGACATATATGATGTTTGTGAAAAATCATTTTCAGGAGTT 8585  
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Qy 2941 ATTGCTTTTGTGTTTCTCTTGGGTTATTAATGTAAGCAGAGGATTTAATCTTAC 3000  
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Qy 3781 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3840  
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Qy 3841 GTATGAGTGAATAATTTGGATGTTCTTTTAAAGAAAACTCCAAACAGATTTCTGAAA 3900  
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Qy 4681 ACCCGAGACACTGCTCCGGGCTGTGCAACAGGCTCAAGAGAAAGTAAAGTCAAGTGG 4740  
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 ; APPLICANT: Nguyen, Thai D.  
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 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-244-633-3  
 Query Match 81.5%; Score 4888.8; DB 5; Length 6169;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 4949; Conservative 0; Mismatches 2; Indels 9; Gaps 5;  
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Oy 481 CTTTCTTCCCTCATCTCATTTTCAGGCTAGTTACCAATTTTATTCACATGCTTTGTG 540  
Db 1696 CTTTCTTCCCTCATCTCATTTTCAGGCTAGTTACCAATTTTATTCACATGCTTTGTG 1755  
Oy 541 GTAAAGCTCCACATGTGTACTGAAATTAAGATATACATAAACTAGTTCCATTTGGGGCA 600  
Db 1756 GTAAAGCTCCACATGTGTACTGAAATTAAGATATACATAAACTAGTTCCATTTGGGGCA 1815  
Oy 601 TCTGTGTGTGTATAGGGGAGAGAGGATACCCGAGAGACTCTTGAAGCCCCGGGAG 660  
Db 1816 TCTGTGTGTGTATAGGGGAGAGAGGATACCCGAGAGACTCTTGAAGCCCCGGGAG 1875  
Oy 661 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTTGGGTCTCTGAGCA 720  
Db 1876 AGGTTTCTCTCAAGCTGGGGAGCCCTGCAAGCACCCGGGGTCTTGGGTCTCTGAGCA 1935  
Oy 721 ACTGCGAGCCCGTGCACCTGGTGTGTTTATATCACTCTCTGAGGACCTGTGCTTTCT 780  
Db 1936 ACTGCGAGCCCGTGCACCTGGTGTGTTTATATCACTCTCTGAGGACCTGTGCTTTCT 1995  
Oy 781 ATTTCTGTGTGACCTGTTCAATTCATCAAGGATTCATTTGACAAATTTATAGTACTTA 840  
Db 1996 ATTTCTGTGTGACCTGTTCAATTCATCAAGGATTCATTTGACAAATTTATAGTACTTA 2055  
Oy 841 TCTGCGAGACACAGAGACAAAATGTGAGCAAGACAGTCACTGCGCTTACCTTCGTGAG 900  
Db 2056 TCTGCGAGACACAGAGACAAAATGTGAGCAAGACAGTCACTGCGCTTACCTTCGTGAG 2115  
Oy 901 GTGACAGTTTCTCATGGAAGAGCTGCGAGAGAAAATTATAGCCAGCCACTTAACCA 960  
Db 2116 GTGACAGTTTCTCATGGAAGAGCTGCGAGAGAAAATTATAGCCAGCCACTTAACCA 2175  
Oy 961 GTGCGAAGAAAGAAATTAACACATCTTGAAATTTGTGGGAGGATCCCTTAACA 1020  
Db 2176 GTGCGAAGAAAGAAATTAACACATCTTGAAATTTGTGGGAGGATCCCTTAACA 2235  
Oy 1021 GGCACACTCCCTAGAGCCCTGCTGCTCCATCTGTGCCGAGGCCCCCAAGCCGAGT 1080  
Db 2236 GGCACACTCCCTAGAGCCCTGCTGCTCCATCTGTGCCGAGGCCCCCAAGCCGAGT 2295  
Oy 1081 CTTCCAGCTCTCTCTCATATGTCACAGCGCTGAGTGGCTGCTGCTTCCCTGTG 1140  
Db 2296 CTTCCAGCTCTCTCTCATATGTCACAGCGCTGAGTGGCTGCTGCTTCCCTGTG 2355  
Oy 1141 AATGCTCCGTGTGATCTGAGCTGGAGACTCCTTGCTCAGGCTCAGAAAGAAATGG 1200  
Db 2356 AATGCTCCGTGTGATCTGAGCTGGAGACTCCTTGCTCAGGCTCAGAAAGAAATGG 2415  
Oy 1201 AGAGGAAACTAGTCTAACGAGAAATCTGAGAGGGACAGTGTTCCTCAGAGGAAAGG 1260  
Db 2416 AGAGGAAACTAGTCTAACGAGAAATCTGAGAGGGACAGTGTTCCTCAGAGGAAAGG 2475  
Oy 1261 GCTCCACGTCGAGAGAAATTCAGAGAGTGGGACTGCGAGAGTGGGAGCGCTGGGCG 1320  
Db 2476 GCTCCACGTCGAGAGAAATTCAGAGAGTGGGACTGCGAGAGTGGGAGCGCTGGGCG 2535  
Oy 1321 TGAAGCGGTGTGAAAGGAGAGAGTGAAGAGGAGCAAGCTGAGAGCTCCAGATGTC 1380  
Db 2536 TGAAGCGGTGTGAAAGGAGAGAGTGAAGAGGAGCAAGCTGAGAGCTCCAGATGTC 2595  
Oy 1381 AGTGTGTTCAAGGAGCTGGAGTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT 1440  
Db 2596 AGTGTGTTCAAGGAGCTGGAGTTTCCGTGCTTCTGTGAGCTTTTATCTTTTCT 2655  
Oy 1441 CTGCTTGAAGAGAGAGATCTATTTTCATGAGAGGATGCAATTCATTAAGTCACTGTT 1500  
Db 2656 CTGCTTGAAGAGAGAGATCTATTTTCATGAGAGGATGCAATTCATTAAGTCACTGTT 2715

Oy 1501 AAAATTCAGAGGTGTGATGGGTTTTCCTTCAAGAAAGCCTTATTTAATGGAAATATAG 1560  
Db 2716 AAAATTCAGAGGTGTGATGGGTTTTCCTTCAAGAAAGCCTTATTTAATGGAAATATAG 2775  
Oy 1561 GAAGCGAGCTCATTTCTAGGCGCTTAATTCACGGAAGAGTGACTGAGATCTTTCTTT 1620  
Db 2776 GAAGCGAGCTCATTTCTAGGCGCGTAAATTCACGGAAGAGTGACTGAGATCTTTCTTT 2835  
Oy 1621 CATGCTTCTGGGCACTACTCAGCCGTTGTGGAATGAGCTATGCAAGAAGGTGAA 1680  
Db 2836 CATGCTTCTGGGCACTACTCAGCCGTTGTGGAATGAGCTATGCAAGAAGGTGAA 2895  
Oy 1681 AACCTGGAATCAGAGACTCGGTTTCTTCTGTTCTGCAATGAGTGTGCTGCGAC 1740  
Db 2896 AACCTGGAATCAGAGACTCGGTTTCTTCTGTTCTGCAATGAGTGTGCTGCGAC 2955  
Oy 1741 CGTGGGCAAGTGTCTCTCTTCCCTGGGCCATATCTTCTCTGATTAAGACCTTGCA 1800  
Db 2956 CGTGGGCAAGTGTCTCTCTTCCCTGGGCCATATCTTCTCTGATTAAGACCTTGCA 3015  
Oy 1801 GCTCTCGTGTCTGTGAACCTTCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGG 1860  
Db 3016 GCTCTCGTGTCTGTGAACCTTCCTGTGATTCCTGTGAGGGGGATGTTGAGAGGG 3075  
Oy 1861 AAGGAGCGAGCTGAGAGACTGAGCCACAGGGAGGTGAGGGGACAGAAAGCAGG 1920  
Db 3076 AAGGAGCGAGCTGAGAGACTGAGCCACAGGGAGGTGAGGGGACAGAAAGCAGG 3135  
Oy 1921 CAGAACTGGGTGCTCCATCATGCTCTCACTGATATCACTGACATCCAGAACCCGAGCA 1980  
Db 3136 CAGAACTGGGTGCTCCATCATGCTCTCACTGATATCACTGACATCCAGAACCCGAGCA 3195  
Oy 1981 CAATGCTTCAGAAAGCTCAATGAACCAACAGCCACTTTCTTCCCTAAGATAGAC 2040  
Db 3196 CAATGCTTCAGAAAGCTCAATGAACCAACAGCCACTTTCTTCCCTAAGATAGAC 3255  
Oy 2041 AATGCAATTTGCAATTAACCAAAAGAAATGAGAGACTAATGAGTGTGCTTTGCTG 2100  
Db 3256 AATGCAATTTGCAATTAACCAAAAGAAATGAGAGACTAATGAGTGTGCTTTGCTG 3315  
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Db 3316 GCATTCAAAACTGGGCGAGAGCAAGTGGAAATGCGAGAAATGTTAACTTTTCAACC 3375  
Oy 2161 TGAACGAGACCCGAGAGCTCAGGAGTGAATGCTGACAGGACGGAAGTGAACCTGAGGC 2220  
Db 3376 TGAACGAGACCCGAGAGCTCAGGAGTGAATGCTGACAGGACGGAAGTGAACCTGAGGC 3435  
Oy 2221 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCAATCAAG 2280  
Db 3436 AGGGAGGAGAAAGAAAGAGAGGATAGTATAGAGCAAGAAAGACAGATTCAATCAAG 3495  
Oy 2281 GGCAGTGGAAATTTGACACAGGATTAATGTCACGTATCTTGCTTCTAGAGGCGAG 2340  
Db 3496 GGCAGTGGAAATTTGACACAGGATTAATGTCACGTATCTTGCTTCTAGAGGCGAG 3555  
Oy 2341 GCTAATTTGGGGGGAATAATCAGTTCAAGGGAAGTCGGGAGACTGATTTCTAATAC 2400  
Db 3556 GCTAATTTGGGGGGAATAATCAGTTCAAGGGAAGTCGGGAGACTGATTTCTAATAC 3615  
Oy 2401 TATATTTTCTTTTCAAGCTGAGTAATTTCTGAGCAATGTCANAGTATGTAATGAGCT 2460  
Db 3616 TATATTTTCTTTTCAAGCTGAGTAATTTCTGAGCAATGTCANAGTATGTAATGAGCT 3675  
Oy 2461 GTAAGATTAATTAATTTCTCTTATTAAGAACTTTTCTCTGTGAGTTAGCAGCA 2520  
Db 3676 GTAAGATTAATTAATTTCTCTTATTAAGAACTTTTCTCTGTGAGTTAGCAGCA 3735  
Oy 2521 AGGCAATCCGTTCTTTTAAACAGAGAAAGAACTCTAAGAGTAAAGCCAAACAGT 2580  
Db 3736 AGGCAATCCGTTCTTTTAAACAGAGAAAGAACTCTTAAAGTTAAAGCCAAACAGT 3795

OY	2581	TCAAACCTAGGCTCTGCACTATATGATGCTTTTGGAAAATCAATTTACAGGATCT	2640
Db	3796	TCAAACCTAAGGCTTGGCACTATATGATGCTTTTGGAAAATCAATTTACAGGATCT	3855
OY	2641	TACTATCTGATTCAGAAAATGAGACTAGTACCCCTTGGCTCAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAAATGAGACTAGTACCCCTTGGCTCAGCTGTAAACAAACCCAG	3915
OY	2701	TTGTAAATGCTCAAGTTCAAGGCTTAACTGCAAGAACCAATCAAAATGAATAGATCTTT	2760
Db	3916	TTGTAAATGCTCAAGTTCAAGGCTTAACTGCAAGAACCAATCAAAATGAATAGATCTTT	3974
OY	2761	AGAGCAAACTGGTTTCTCCAC-TCGTGAGGTGAGTCTGCCAGGGCAGTTTGGAAATTT	2819
Db	3975	AGAGCAAACTGGTTTCTCCACATCTGAGGTGAGTCTGCCAGGGCAGTTTGGAAATTT	4034
OY	2820	TACTTCACAAGATTTGACACTGTTGGTATTAACAACATAAAGTTGCTCAAAAGGCAAT	2879
Db	4035	TACTTCACAAGATTTGACACTGTTGGTATTAACAACATAAAGTTGCTCAAAAGGCAAT	4094
OY	2880	CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATATTTATTTGCTATATGC	2939
Db	4095	CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTGGTATATTTATTTGCTATATGC	4154
OY	2940	CATTTCCTTTTGTGTTTTCTCTTGGGTTATTAATGTAAAGAGGGATTTATTAACCTA	2999
Db	4155	CATTTCCTTTTGTGTTTTCTCTTGGGTTATTAATGTAAAGAGGGATTTATTAACCTA	4214
OY	3000	CAGTCCAGAAAGCCTGGAATTTGGAATGAGAAAAATTAACATTTTGTGTTTCCACCT	3059
Db	4215	CAGTCCAGAAAGCCTGGAATTTGGAATGAGAAAAATTAACATTTTGTGTTTCCACCT	4274
OY	3060	TCTAATAATTTAAACATTTTATTCATTTGCGAATGAGCCATTAACCTCAAGTGGTAAT	3119
Db	4275	TCTAATAATTTAAACATTTTATTCATTTGCGAATGAGCCATTAACCTCAAGTGGTAAT	4334
OY	3120	AACGATACCTGTGATTTGTCAATTAACCAATGAAATCAACAGCATTTTATATCTATATAC	3179
Db	4335	AACGATACCTGTGATTTGTCAATTAACCAATGAAATCAACAGCATTTTATATCTATATAC	4394
OY	3180	AGTGTGCGAATACGTTGTAAGGAAATATTTATCTCAAAACTACTTTGAAATTGAC	3239
Db	4395	AGTGTGCGAATACGTTGTAAGGAAATATTTATCTCAAAACTACTTTGAAATTGAC	4454
OY	3240	CTCTGTGCGATCTTGTGTTTTAACATATTAATAAATGTTTAAATTTTGAATATTTG	3299
Db	4455	CTCTGTGCGATCTTGTGTTTTAACATATTAATAAATGTTTAAATTTTGAATATTTG	4514
OY	3300	ATAATCATATTTCAATATCATTTGTTTCTTGTAACTATATTTTATATATTGAAATAC	3359
Db	4515	ATAATCATATTTCAATATCATTTGTTTCTTGTAACTATATTTTATATATTGAAATAC	4574
OY	3360	ATCTTTTCGAAAGATTCCTCCCAATTTTCAATGAGGTTCTTGGATGCAACACACA	3419
Db	4575	ATCTTTTCGAAAGATTCCTCCCAATTTTCAATGAGGTTCTTGGATGCAACACACA	4634
OY	3420	GAGTAAAGAACTGATTTAGAGGCTTAACATTTGATGAGGCTGAGATGCAAGACTGAAT	3479
Db	4635	GAGTAAAGAACTGATTTAGAGGCTTAACATTTGATGAGGCTGAGATGCAAGACTGAAT	4694
OY	3480	TAGAAAGTCTCCCAAAAGATCAACAGTTGTTTTAAAGCTAGGGGTGAAGGGGGAATCTG	3539
Db	4695	TAGAAAGTCTCCCAAAAGATCAACAGTTGTTTTAAAGCTAGGGGTGAAGGGGGAATCTG	4754
OY	3540	CCGCTCTCATATGGAATCTCTCCCTGGAAGCTGTAAGGTTGCTGTCTTGTGTTCTGGCT	3599
Db	4755	CCGCTCTCATATGGAATCTCTCCCTGGAAGCTGTAAGGTTGCTGTCTTGTGTTCTGGCT	4814
OY	3600	GGCTGTATATTTTCTCTGCTCCCTGCTAAGCTTAAAGAACTGTTTGAATCTCAAGTTC	3659
Db	4815	GGCTGTATATTTTCTCTGCTCCCTGCTAAGCTTAAAGAACTGTTTGAATCTCAAGTTC	4874
OY	3660	TAGCATATGCTCTGCAACAGTGCAGGTTCTCAATAGATTTTGGACAGATGAAATGAATATA	3719

[illegible]

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Db      5955 TGGGGGAGCTGAGTTCAGAGGATATAGCTGTAGTACCTGCTACAGGCGCTCCA 6014
Qy      4798 GAGCTCCCTGCTGCTCTTCTCTAGAGACTGCACAGTACACAGATGAATTA 4857
Db      6015 GGGCTC---CCTGCGCTTTCTCTAGAGACTGCACAGTACAGATGAATTA 6070
Qy      4858 AGGAAAGACAGAGATCACTTCAAGTATTAAGTAAATTTAGCTCTGAGAGCTTCAAT 4917
Db      6071 AGGAAAGACACACATCACTTCAAGTATTAAGTAAATTTAGCTCTGAGAGCTTCAAT 6129
Qy      4918 TAGATTAGTGTTCAGAGTCTTGTGCCCCCTCCAGTCAAG 4957
Db      6130 TAGATTAGTGTTCAGAGTCTTGTGCCCCCTCCAGTCAAG 6169

RESULT 4
US-09-985-637A-1
; Sequence 1, Application US/09985637A
; Publication No. US20030119000A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PROH
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
; PILE REFERENCE: 13587,296
; CURRENT APPLICATION NUMBER: US/09/985,637A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-985-637A-1

Query Match      67.8%; Score 4069.4; DB 3; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4082; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy      1 GCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCATCAGATGTTTACAGCCAGAGACTC 60
Db      1216 GCTCCACAGAGAGTCTCCCACTCTAGACTTCTGCATCAGATGTTTACAGCCAGAGACTC 1275
Qy      61 CGTGAAGGTGAGGGTCTGTGTCTTACACCTTACCTGTATGCTGTACACTGAGCTCACTGC 120
Db      1276 CGTGAAGGTGAGGGTCTGTGTCTTACACCTTACCTGTATGCTGTACACTGAGCTCACTGC 1335
Qy      121 AACCTCTGCTCTCCAGGTTCAAGCAATTTCTCTGTCTCAGCCTCCCGCTACTGGAGCT 180
Db      1336 AACCTCTGCTCTCCAGGTTCAAGCAATTTCTCTGTCTCAGCCTCCCGCTACTGGAGCT 1395
Qy      181 ACAGGCGACGCGCCGGCTAATTTTGTATTTAGTATGAGATGAGGTTTACCATTTAG 240
Db      1396 ACAGGCGACGCGCCGGCTAATTTTGTATTTAGTATGAGATGAGGTTTACCATTTAG 1455
Qy      241 CCGGCTGTGCTTGAATCTCTGACCTCAAGTGAATCCACCCACCTCAGCTCTCTAAAGTGC 300
Db      1456 CCGGCTGTGCTTGAATCTCTGACCTCAAGTGAATCCACCCACCTCAGCTCTCTAAAGTGC 1515
Qy      301 TGGGATTAACAGCATATGATCAACGCGCGCCGCGCAAGGCTCAGTGTATTAAGAAATAC 360
Db      1516 TGGGATTAACAGCATATGATCAACGCGCGCCGCGCAAGGCTCAGTGTATTAAGAAATAC 1575
Qy      361 TGGATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATTTTTCAGGAAATTC 420
Db      1576 TGGATGTGTTTACTAAACCAACAGGAAACAGACAAAGCTGTGATTTTTCAGGAAATTC 1635
Qy      421 TTGGATGAGGAAATGATGTCATGAGTGCCTGTGCTAGTCCACAGACCACTGTCTTCATCA 480
Db      1636 TTGGATGAGGAAATGATGTCATGAGTGCCTGTGCTAGTCCACAGACCACTGTCTTCATCA 1695
Qy      481 CTTTCTTCCCTCATCTCTCATTTTTCAGGCTTAAGTATACATTTTATTCACATGCTTTTGTG 540
Db      1696 CTTTCTTCCCTCATCTCTCATTTTTCAGGCTTAAGTATACATTTTATTCACATGCTTTTGTG 1755

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Qy      541 GTAACTCTCACAATGTTACTGAATAAGATATACATAAATAGTTCCATTTTGGGCGCA 600
Db      1756 GTAACTCTCACAATGTTACTGAATAAGATATACATAAATAGTTCCATTTTGGGCGCA 1815
Qy      601 TCTGTGTGTGTGTATAGGAGAGAGGGGCTATCCCAAGAGACTCTTGAAGCCCCCGGAG 660
Db      1816 TCTGTGTGTGTGTATAGGAGAGAGGGGCTATCCCAAGAGACTCTTGAAGCCCCCGGAG 1875
Qy      661 AGGTTTCCCTCCAGCTGGGGGAGCCCTGCAGAGACCCGGGGGTCTGGGTGTCTGTAGCA 720
Db      1876 AGGTTTCCCTCCAGCTGGGGGAGCCCTGCAGAGACCCGGGGGTCTGGGTGTCTGTAGCA 1935
Qy      721 ACCTGCAGCCCGTGCACATGTTGTTTGTATCACTCTGTAGGACCTGTGCTTTCT 780
Db      1936 ACCTGCAGCCCGTGCACATGTTGTTTGTATCACTCTGTAGGACCTGTGCTTTCT 1995
Qy      781 ATTTCTGTGTGATCTGTTCATTTCAATCCAGGATTCATTCACATTTTATAGTACTTATA 840
Db      1996 ATTTCTGTGTGATCTGTTCATTTCAATCCAGGATTCATTCACATTTTATAGTACTTATA 2055
Qy      841 TCTGCAGACACACAGACCAAAATGTGAGCAAGAGTCACTGCCCTACCTTGTGAG 900
Db      2056 TCTGCAGACACACAGACCAAAATGTGAGCAAGAGTCACTGCCCTACCTTGTGAG 2115
Qy      901 GTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAATTAATAGCAAGCCACTTAACCCA 960
Db      2116 GTGACAGTTTCTCATGGAAGACGTGCAGAGAGAAATTAATAGCAAGCCACTTAACCCA 2175
Qy      961 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGGCCCAAGATATCCCTTAACA 1020
Db      2176 GTGCTGAAGAAAGAAATTAACACATCTTGAAGAAATTTGGCCCAAGATATCCCTTAACA 2235
Qy      1021 GGGCAACCTCCCTAGAGCCCGCTGCTGCTCCATGCTGTCGCGGAGGCCCCCAAGCCGAGT 1080
Db      2236 GGGCAACCTCCCTAGAGCCCGCTGCTGCTCCATGCTGTCGCGGAGGCCCCCAAGCCGAGT 2295
Qy      1081 CTTCCAGCCTCTCTCTCCATCAATGATCAGGCTGCAGCTGAGCTGCTGCTTCCCGTG 1140
Db      2296 CTTCCAGCCTCTCTCTCCATCAATGATCAGGCTGCAGCTGAGCTGAGCTGCTTCCCGTG 2355
Qy      1141 AATGCTCTGTGATCTGAGCTGAGATCTCTTGTGCTCCAGGCTCCAGAAAGAAATAG 1200
Db      2356 AATGCTCTGTGATCTGAGCTGAGATCTCTTGTGCTCCAGGCTCCAGAAAGAAATAG 2415
Qy      1201 AGAGGAAACTAGTCTAACGAGAAATCTGAGGGGACAGTGTTCCTCAGAGGGAAAGG 1260
Db      2416 AGAGGAAACTAGTCTAACGAGAAATCTGAGGGGACAGTGTTCCTCAGAGGGAAAGG 2475
Qy      1261 GCTTCACAGTCCAGAGAAATTCAGAGAGTGGGACCTGCAGAGAGTGGGAGCGCTGGGAC 1320
Db      2476 GCTTCACAGTCCAGAGAAATTCAGAGAGTGGGACCTGCAGAGAGTGGGAGCGCTGGGAC 2535
Qy      1321 TGAAGGAGTCTGAAGGCAAGAGGTGAAGAGGCAAGGCTGAAAGCTGCCAATGTTTC 1380
Db      2536 TGAAGGAGTCTGAAGGCAAGAGGTGAAGAGGCAAGGCTGAAAGCTGCCAATGTTTC 2595
Qy      1381 AGTGTGTTCAAGGGGCTGGGAGTTTCCGTTGCTCTCTGAGAGCTTTTATCTTTTCT 1440
Db      2596 AGTGTGTTCAAGGGGCTGGGAGTTTCCGTTGCTCTCTGAGAGCTTTTATCTTTTCT 2655
Qy      1441 CTGCTTGAAGAGAGAAAGTCTAATTCATGAAGGATCAGTTTCAATAAGCTCAGCTGT 1500
Db      2656 CTGCTTGAAGAGAGAAAGTCTAATTCATGAAGGATCAGTTTCAATAAGCTCAGCTGT 2715
Qy      1501 AAAATTCAGAGGTGATAGGTTTCTTTCACAGAGGCTTTATTTAATGGAATATAG 1560
Db      2716 AAAATTCAGAGGTGATAGGTTTCTTTCACAGAGGCTTTATTTAATGGAATATAG 2775
Qy      1561 GAAAGCACTCATTTCCAGGCGGTTAATTCACGGAAGAGTCACTGAGCTTTTCTTT 1620
Db      2776 GAAAGCACTCATTTCCAGGCGGTTAATTCACGGAAGAGTCACTGAGCTTTTCTTT 2835

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QY	1621	CATGCTCTGGGCAACTACAGCCCTGTGTGACCTTGGCTTATGCAACGGTCGA	1680
Db	2836	CATGCTCTGGGCAACTACAGCCCTGTGTGACCTTGGCTTATGCAACGGTCGA	2895
QY	1681	AACCTTGGANATCAGAGACCTCGGTTTCTTCTGTGGTCTGCAATGTGTGGCTGCGAC	1740
Db	2896	AACCTTGGANATCAGAGACCTCGGTTTCTTCTGTGGTCTGCAATGTGTGGCTGCGAC	2955
QY	1741	CGTGGCAAGTGTCTCTCCCTTCCCTGGCCATAGTCTTCTGTATTAAGACCCCTTCA	1800
Db	2956	CGTGGCAAGTGTCTCTCCCTTCCCTGGCCATAGTCTTCTGTATTAAGACCCCTTCA	3015
QY	1801	GCTCTCGTGTCTGTGAACACTTCCCTGTGATCTCTGTGAGGGGGCATGTTGAGAGGG	1860
Db	3016	GCTCTCGTGTCTGTGAACACTTCCCTGTGATCTCTGTGAGGGGGCATGTTGAGAGGG	3075
QY	1861	AAGAGGCAAGCTGAGGAGCTGAGCCACAGGGGAGGTGAGGGGGGACAGAAAGGACG	1920
Db	3076	AAGAGGCAAGCTGAGGAGCTGAGCCACAGGGGAGGTGAGGGGGGACAGAAAGGACG	3135
QY	1921	CAGAACTGGGTGCTCATCAGTCTCTCATCTGATCAGTCAAGTCCAGAACCGAGACCA	1980
Db	3136	CAGAACTGGGTGCTCATCAGTCTCTCATCTGATCAGTCAAGTCCAGAACCGAGACCA	3195
QY	1981	CAATGCTTCAAGAAAGCTCAATGAACCCACACGCCACTTTTCTTCCCTTAAGCATAGAC	2040
Db	3196	CAATGCTTCAAGAAAGCTCAATGAACCCACACGCCACTTTTCTTCCCTTAAGCATAGAC	3255
QY	2041	AATGSCATTTGGCCAAATAACAAAGATGAGAGACATACTGGGTGAGCTTTGGCTG	2100
Db	3256	AATGSCATTTGGCCAAATAACAAAGATGAGAGACATACTGGGTGAGCTTTGGCTG	3315
QY	2101	GCATTCAAAAACTGGGCCAGAGCAAGTGGAAAAATGCCAGAGATTGTTAACTTTTCAACC	2160
Db	3316	GCATTCAAAAACTGGGCCAGAGCAAGTGGAAAAATGCCAGAGATTGTTAACTTTTCAACC	3375
QY	2161	TGACACAGACCCCAACGACCTCAGACGTGACTGTGACAGCACGAGTGAACCTGACGGC	2220
Db	3376	TGACACAGACCCCAACGACCTCAGACGTGACTGTGACAGCACGAGTGAACCTGACGGC	3435
QY	2221	AGGGGAGGAGAAAAAGAGGGGATGTGTATGACGAAGACAAAGACAGATTCAATTAAG	2280
Db	3436	AGGGGAGGAGAAAAAGAGGGGATGTGTATGACGAAGACAAAGACAGATTCAATTAAG	3495
QY	2281	GGCAGTGGGAATTGACACACAGGGAATTATGTCACGTAATCTTGGGTTCTTAGAGGACGG	2340
Db	3496	GGCAGTGGGAATTGACACACAGGGAATTATGTCACGTAATCTTGGGTTCTTAGAGGACGG	3555
QY	2341	GCTATATTGTGGGGGAAAAAATCATGTTCAAGGAAAGTCGGAGACCTGATTTCTAATAC	2400
Db	3556	GCTATATTGTGGGGGAAAAAATCATGTTCAAGGAAAGTCGGAGACCTGATTTCTAATAC	3615
QY	2401	TATATTTTTCTTTTACAAGCTGATTAATTCTGACCAAGTCAACAGGTAATCTGAGGCT	2460
Db	3616	TATATTTTTCTTTTACAAGCTGATTAATTCTGACCAAGTCAACAGGTAATCTGAGGCT	3675
QY	2461	GTAAGATTACTTAAGTTCTCTCTATTAGGAACCTTTTTCTCTGTGAGTTAGACAGACA	2520
Db	3676	GTAAGATTACTTAAGTTCTCTCTATTAGGAACCTTTTTCTCTGTGAGTTAGACAGACA	3735
QY	2521	AGGGCAATCCCGTTCTTTTAAACAGAGAAACAATTCCTAAGATGAAGCCAAACAGAT	2580
Db	3736	AGGGCAATCCCGTTCTTTTAAACAGAGAAACAATTCCTAAGATGAAGCCAAACAGAT	3795
QY	2581	TCAAGCCTAGGCTTGGCGCATATATATGTGTTTTTGAAAAATCATTTCAAGGAAGTT	2640
Db	3796	TCAAGCCTAGGCTTGGCGCATATATATGTGTTTTTGAAAAATCATTTCAAGGAAGTT	3855
QY	2641	TACTATCTGATTCAGAAATATGACATGATACCTTTGGTCAGCTGTAAACAAACCCAT	2700
Db	3856	TACTATCTGATTCAGAAATATGACATGATACCTTTGGTCAGCTGTAAACAAACCCAT	3915
QY	2701	TTGTAAATGTCTCAAGTTCAGGCTTAACTGACAGAACCAATCAATAAAGAAATAGATCTTT	2760

[illegible]





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Db 2596 AGTGTGTTACGCGGCTGGAGATTTCGCTGCTTCCTGAGACCTTTTATCTTTCT 2555  
QY 1441 CTGCTTGGAGAGAAAGATCTATTTCATGAAGGATGCACTTTTCAATAAGTCACTGTT 1500  
Db 2656 CTGCTTGGAGAGAAAGATCTATTTCATGAAGGATGCACTTTTCAATAAGTCACTGTT 2715  
QY 1501 AAAATTCAGGCTGTGATGGGATTTTCTTACGAAAGGCTTTTATTTAATGGGAATATAG 1560  
Db 2716 AAAATTCAGGCTGTGATGGGATTTTCTTACGAAAGGCTTTTATTTAATGGGAATATAG 2775  
QY 1561 GAAGCAGATCTATTCTTCTAGCCGCTTAATCACGGAAGAGTGACTGAGTCTTTTCTTT 1620  
Db 2776 GAAGCAGATCTATTCTTCTAGCCGCTTAATCACGGAAGAGTGACTGAGTCTTTTCTTT 2835  
QY 1621 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGACTTGGCTTTATGCAAGCGTGGAA 1680  
Db 2836 CATGCTTCTGGGCAACTACTCAGCCCTGTGTGACTTGGCTTTATGCAAGCGTGGAA 2895  
QY 1681 AACCTTGAATCAGAGACTCGGTTTTCTTCTGTTTCTGSCAATGGTTGGCTGTGGAC 1740  
Db 2896 AACCTTGAATCAGAGACTCGGTTTTCTTCTGTTTCTGSCAATGGTTGGCTGTGGAC 2955  
QY 1741 CGTGGCAAGTGTCTCTCTTCCCTGGCCATAGTCTTCTGTCTATAAAGACCTTGTCA 1800  
Db 2956 CGTGGCAAGTGTCTCTCTTCCCTGGCCATAGTCTTCTGTCTATAAAGACCTTGTCA 3015  
QY 1801 GCTCTGTGTCTGTGAACTTCCCTGTGATTTCTGTGAGGGGGAGTTGAGAGGG 1860  
Db 3016 GCTCTGTGTCTGTGAACTTCCCTGTGATTTCTGTGAGGGGGAGTTGAGAGGG 3075  
QY 1861 AAGGAGCAGAGCTGAGAGCTGAGCCACAGGGGAGTGGAGAGGGGAGAGAGGACAG 1920  
Db 3076 AAGGAGCAGAGCTGAGAGCTGAGCCACAGGGGAGTGGAGAGGGGAGAGAGGACAG 3135  
QY 1921 CAGAACTGGGTGCTCATCACTGCTCACTGATCAGTCACTGAGTCCAGAGCCGAGAGCCA 1980  
Db 3136 CAGAACTGGGTGCTCATCACTGCTCACTGATCAGTCACTGAGTCCAGAGCCGAGAGCCA 3195  
QY 1981 CATGCTTCAAGAAAGCTCAATGAAACCAACAGCCACATTTTCTTCCCTAAGCATATGAC 2040  
Db 3196 CATGCTTCAAGAAAGCTCAATGAAACCAACAGCCACATTTTCTTCCCTAAGCATATGAC 3255  
QY 2041 AATGGCAATTGGCAATATACAAAGAAATGAGAGAGCTAATGCTGTGCTTTTCCCTG 2100  
Db 3256 AATGGCAATTGGCAATATACAAAGAAATGAGAGAGCTAATGCTGTGCTTTTCCCTG 3315  
QY 2101 GCATTCAAAAACCTGGGCTCAGAGCAAGTGGAAATGCGCAGAGATTGTTAACTTTTCAACC 2160  
Db 3316 GCATTCAAAAACCTGGGCTCAGAGCAAGTGGAAATGCGCAGAGATTGTTAACTTTTCAACC 3375  
QY 2161 TGAACGACACCCACGAGCTCAGAGTGACTGTGACAGACAGAGTGAACCTGCAAGCC 2220  
Db 3376 TGAACGACACCCACGAGCTCAGAGTGACTGTGACAGACAGAGTGAACCTGCAAGCC 3435  
QY 2221 AAGGGAGAGAGAAAGAAAGAGGGATATGTTATGAGCAAGAAAGCAATTCATTCAAG 2280  
Db 3436 AAGGGAGAGAGAAAGAAAGAGGGATATGTTATGAGCAAGAAAGCAATTCATTCAAG 3495  
QY 2281 GGCAGTGGAAATTGACACAGGAGTTATAGTCAAGTATCTGGGTTCTAAGAGGCAAG 2340  
Db 3496 GGCAGTGGAAATTGACACAGGAGTTATAGTCAAGTATCTGGGTTCTAAGAGGCAAG 3555  
QY 2341 GCTATATTTGTGGGGGAAAAAATCAGTTCAAGGGAAATGGGAGACCTGATTTCTAATAC 2400  
Db 3556 GCTATATTTGTGGGGGAAAAAATCAGTTCAAGGGAAATGGGAGACCTGATTTCTAATAC 3615  
QY 2401 TATATTTTCTTTTCAAGCTAGTAACTCTGAGCAAGTCAAGATATTAATCTAGAGCT 2460  
Db 3616 TATATTTTCTTTTCAAGCTAGTAACTCTGAGCAAGTCAAGATATTAATCTAGAGCT 3675  
QY 2461 GTAAGATTACTAGTTTCTCTTATTAGAACTCTTTTCTCTGTGAGATTAGACAGACA 2520

Db 3676 GTAAGATTACTAGTTTCTCTTATTAGAACTTTTCTCTGTGAGATTAGACAGACA 3735  
QY 2521 AGGGCAATCCGTTTCTTTTAAACAGAGAAAAATCTCTAAGATTAAGCCAAACAGAT 2580  
Db 3736 AGGGCAATCCGTTTCTTTTAAACAGAGAAAAATCTCTAAGATTAAGCCAAACAGAT 3795  
QY 2581 TCAAGCTTAAAGTCTGTGCTGATATGATTTGTTTTTGAATAATCAATTCACCGATGT 2640  
Db 3796 TCAAGCTTAAAGTCTGTGCTGATATGATTTGTTTTTGAATAATCAATTCACCGATGT 3855  
QY 2641 TACTATCTGATTCAAGAAATGAGACTAGTACCCTTGTGCTGATTAACAAACACCCAT 2700  
Db 3856 TACTATCTGATTCAAGAAATGAGACTAGTACCCTTGTGCTGATTAACAAACACCCAT 3915  
QY 2701 TTGTAAATGTCTCAAGTTCAGGCTTAAGTCAAGAACCAATCAATTAAGATATGATCTTT 2760  
Db 3916 TTGTAAATGTCTCAAGTTCAGGCTTAAGTCAAGAACCAATCAATTAAGATATGATCTTT 3975  
QY 2761 AAGAGAACTGTGTTTCTCCACTCTGAGAGTGAAGTCTGCAAGGCACTTTGGAATATTT 2820  
Db 3976 AAGAGAACTGTGTTTCTCCACTCTGAGAGTGAAGTCTGCAAGGCACTTTGGAATATTT 4035  
QY 2821 ACTTCAAGATTTGACACTGTGTTGATTAACAACATAAAGTTGCTCAAGGCAATC 2880  
Db 4036 ACTTCAAGATTTGACACTGTGTTGATTAACAACATAAAGTTGCTCAAGGCAATC 4095  
QY 2881 ATTATTTCAAGTGGCTTAAAGTAACTTCTGACAGTTTGGTATATTTATGCTATTTGCC 2940  
Db 4096 ATTATTTCAAGTGGCTTAAAGTAACTTCTGACAGTTTGGTATATTTATGCTATTTGCC 4155  
QY 2941 ATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAGCAGGATTAATTAACCTAC 3000  
Db 4156 ATTTGCTTTTGTGTTTTTCTCTTGGGTTATTAATGTAAGCAGGATTAATTAACCTAC 4215  
QY 3001 AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTAATTTGTTTTTACACCTT 3060  
Db 4216 AGTCCAGAAAGCCTGTGAATTTGAATGAGAAAAAATTAATTTGTTTTTACACCTT 4275  
QY 3061 CTAACTAAATTTTAACTTTTATTCATTCGAAATGAGCCATTAACCTAAGTGTATATA 3120  
Db 4276 CTAACTAAATTTTAACTTTTATTCATTCGAAATGAGCCATTAACCTAAGTGTATATA 4335  
QY 3121 ACAATGCTGTGATTTTGTCAATTAACATTAAGAAATCAAGACATTTTATCTATATTA 3180  
Db 4336 ACAATGCTGTGATTTTGTCAATTAACATTAAGAAATCAAGACATTTTATCTATATTA 4395  
QY 3181 GTTGTGAGATACGTGTGAAGTGAATATTTATCTCAAAAATCTTGAATTAAGACC 3240  
Db 4396 GTTGTGAGATACGTGTGAAGTGAATATTTATCTCAAAAATCTTGAATTAAGACC 4455  
QY 3241 TCTGCTGATCTTGTGTTTTTAAACATATTAATTAACATGTTTTAAATTTGATATTTGA 3300  
Db 4456 TCTGCTGATCTTGTGTTTTTAAACATATTAATTAACATGTTTTAAATTTGATATTTGA 4515  
QY 3301 TATATCATTTTCAATTAATCAATTTGTTTCTTTGTAATCTATATTTTATATTTGAAAA 3360  
Db 4516 TATATCATTTTCAATTAATCAATTTGTTTCTTTGTAATCTATATTTTATATTTGAAAA 4575  
QY 3361 TCTTTCTGAGAAAGTTCGCCAGATTTCAACAATGAGGTTCTGTGCAAGCAACAAG 3420  
Db 4576 TCTTTCTGAGAAAGTTCGCCAGATTTCAACAATGAGGTTCTGTGCAAGCAACAAG 4635  
QY 3421 AGTAAGAACTGATTTAGAGCTTAACATTTGACATTTGTGCTGAGATGCAAGCTGAATTT 3480  
Db 4636 AGTAAGAACTGATTTAGAGCTTAACATTTGACATTTGTGCTGAGATGCAAGCTGAATTT 4695  
QY 3481 AGAAAGTCTCCCAAGATTAACAAGTTGTTTTTAAAGCTAGAGGCTGAGGGGAAATCTG 3540  
Db 4696 AGAAAGTCTCCCAAGATTAACAAGTTGTTTTTAAAGCTAGAGGCTGAGGGGAAATCTG 4755  
QY 3541 CGCTTCTATAGGAATGCTCTCCCTGAGCCTGATAGGGTGTGCTGTTGCTGAGCTG 3600

[illegible]

Db	1336	AACCTCTCCTCCAGGTTCAAGCAATTCCTCTCTCTCAAGCTCCCGGTAAGCTGGGAACT	1395
Qy	181	AACAGCGACGCCCGGCTAATTTTGTATGTAGTAGAGATGGGGTTTCAACATATTAG	240
Db	1396	AACAGCGCACGCCCGGCTAATTTTGTATGTAGTAGAGATGGGGTTTCAACATATTAG	1455
Qy	241	CCCGGCTGGTCTTGAACTCTCGACTCAAGTGATATCCCACTCAGCTCTCTTAAGTGC	300
Db	1456	CCCGGCTGGTCTTGAACTCTCGACTCAAGTGATATCCCACTCAGCTCTCTTAAGTGC	1515
Qy	301	TGGATATCAGGCAATGATGCACCGCGCCCGGCCAAGGGTCAGTGTTTAATTAAGAAATAC	360
Db	1516	TGGATATCAGGCAATGATGCACCGCGCCCGGCCAAGGGTCAGTGTTTAATTAAGAAATAC	1575
Qy	361	TTGAATGGTTTACTAAACCAACAGGAAACAGACAAAAGCTGTGATTAATTCAGGAAATTC	420
Db	1576	TTGAATGGTTTACTAAACCAACAGGAAACAGACAAAAGCTGTGATTAATTCAGGAAATTC	1635
Qy	421	TTGGGATGGGGAATGGTGCATGAGCTGCCCTGCTTAATGCCAGACATCGTCTCTATCA	480
Db	1636	TTGGGATGGGGAATGGTGCATGAGCTGCCCTGCTTAATGCCAGACATCGTCTCTATCA	1695
Qy	481	CTTTCCTCCCTCATCTCATATTTTCAAGCTAAGTACCATTTTATTCACATGCTTTGTG	540
Db	1696	CTTTCCTCCCTCATCTCATATTTTCAAGCTAAGTACCATTTTATTCACATGCTTTGTG	1755
Qy	541	GTAAAGCTTCCACATGCTTAAGTAATGAATTAACATTAACATGATTCATTGGGGCCA	600
Db	1756	GTAAAGCTTCCACATGCTTAAGTAATGAATTAACATTAACATGATTCATTGGGGCCA	1815
Qy	601	TCTGTGTGTGTGTATAGGGGAGAGAGGGATATCCCAAGACATCTCTTAAGGCCCGGGCAG	660
Db	1816	TCTGTGTGTGTGTATAGGGGAGAGAGGGATATCCCAAGACATCTCTTAAGGCCCGGGCAG	1875
Qy	661	AGGTTTCCTTCACGCTGGGGGAGGCCCTGCAAGACCCCGGGGCTCTGGAGTCTCTGAGCA	720
Db	1876	AGGTTTCCTTCACGCTGGGGGAGGCCCTGCAAGACCCCGGGGCTCTGGAGTCTCTGAGCA	1935
Qy	721	ACCTGCCAGCCCGTGCACATGGTGTGTGTATATCACTCTTAAGGAACCTGTTCCTTCT	780
Db	1936	ACCTGCCAGCCCGTGCACATGGTGTGTGTATATCACTCTTAAGGAACCTGTTCCTTCT	1995
Qy	781	AATTCGTGTGTGACTCGTTCATTCATCCAGGCAATTCATGAACATTTATTAAGTACTTATA	840
Db	1996	AATTCGTGTGTGACTCGTTCATTCATCCAGGCAATTCATGAACATTTATTAAGTACTTATA	2055
Qy	841	TCTGCCACACACCAAGACAAATGGTAGCAAAAGCACTGCCTGCCATCCCTGGTAG	900
Db	2056	TCTGCCACACACCAAGACAAATGGTAGCAAAAGCACTGCCTGCCATCCCTGGTAG	2115
Qy	901	GTGACAGTTCATCATGGAAGAGCTGACAAAGAAATTAATAGCCAGCCAACTTAAACCA	960
Db	2116	GTGACAGTTCATCATGGAAGAGCTGACAAAGAAATTAATAGCCAGCCAACTTAAACCA	2175
Qy	961	GTGCTGAAAAAGAAATTAACACCATCTTGAAGATTGTGCGAGCATCCCTTAACA	1020
Db	2176	GTGCTGAAAAAGAAATTAACACCATCTTGAAGATTGTGCGAGCATCCCTTAACA	2235
Qy	1021	GGGCACTTCCCTTAGGCCCCCTGCTGCCTCATCTGTGCCGGAAGGCCCAAGCCGAGT	1080
Db	2236	GGGCACTTCCCTTAGGCCCCCTGCTGCCTCATCTGTGCCGGAAGGCCCAAGCCGAGT	2295
Qy	1081	CTTCCAAAGCCTCTCCTCATCATAGTCACAGCGCTCAGCTGGCTCGCTTCCCGTG	1144
Db	2296	CTTCCAAAGCCTCTCCTCATCATAGTCACAGCGCTCAGCTGGCTCGCTTCCCGTG	2355
Qy	1141	AATCGTCTTGATGCACTTGAGCTGAGACTCTTGGCTTCAGAGCTCCAGAAAGAAATGG	1200
Db	2356	AATCGTCTTGATGCACTTGAGCTGAGACTCTTGGCTTCAGAGCTCCAGAAAGAAATGG	2415
Qy	1201	AGAGGGAACATGATCTAACGAGAAATCTGAGAGGGAACAGTGTTCCTCAAGGGAAGAGG	1266

Db 2416 AGAGGAAACTAGTCTAACGGAATCTGAGGGGACAGTGTTCCTCAGAGGGAAAGG 2475  
 QY 1261 GCCTCCACGTCAGAGAAATTCAGAGAGTGGGACCTGACGAGAGTGGGACGCTGGGGC 1320  
 Db 2476 GCCTCCACGTCAGAGAAATTCAGAGAGTGGGACCTGACGAGAGTGGGACGCTGGGGC 2535  
 QY 1321 TGAAGCGGTGCTGAAAGGACGAGAAAGTGAAGGGGCAAGGCTGAAGCTGCGCAGATGTT 1380  
 Db 2536 TGAAGCGGTGCTGAAAGGACGAGAAAGTGAAGGGGCAAGGCTGAAGCTGCGCAGATGTT 2595  
 QY 1381 AGAGTGTTCACGGGGCTGGGAATTTCCGTGCTTCCTGAGCCCTTTTATCTTTTCT 1440  
 Db 2596 AGAGTGTTCACGGGGCTGGGAATTTCCGTGCTTCCTGAGCCCTTTTATCTTTTCT 2655  
 QY 1441 CTGCTTGAAGAGAAAGTCTATTCATGAAGGAGTGCAGTTTCAATAAGCAGCTTT 1500  
 Db 2656 CTGCTTGAAGAGAAAGTCTATTCATGAAGGAGTGCAGTTTCAATAAGCAGCTTT 2715  
 QY 1501 AAAATTCAGAGGTGTGCAATGGATTTTCCTTACGAAAGCCTTTATTTAATGGAAATAG 1560  
 Db 2716 AAAATTCAGAGGTGTGCAATGGATTTTCCTTACGAAAGCCTTTATTTAATGGAAATAG 2775  
 QY 1561 GAAAGCAGTCTATTTCTTGAAGCCGTTAATTCAGGAAAGTGAAGTGAAGTCTTTTCTTT 1620  
 Db 2776 GAAAGCAGTCTATTTCTTGAAGCCGTTAATTCAGGAAAGTGAAGTGAAGTCTTTTCTTT 2835  
 QY 1621 CATGCTTCTGAGCACTACTCAGCCCTGAGTGAAGTCTTGAAGGAGGAGTGAAGGAGG 1680  
 Db 2836 CATGCTTCTGAGCACTACTCAGCCCTGAGTGAAGTCTTGAAGGAGGAGTGAAGGAGG 2895  
 QY 1681 AACCTTGAATCAGAGAGTCTGGTTTCTTCTGATTCGCAATGGTGGCTGTCGAC 1740  
 Db 2896 AACCTTGAATCAGAGAGTCTGGTTTCTTCTGATTCGCAATGGTGGCTGTCGAC 2955  
 QY 1741 CGTGGCAAGTGTCTCTCTCTCTCTGGGCAATGTTCTTCTGCTAATAAAGCCTTGA 1800  
 Db 2956 CGTGGCAAGTGTCTCTCTCTCTGGGCAATGTTCTTCTGCTAATAAAGCCTTGA 3015  
 QY 1801 GCTCTGCTTCTGTAACACTTCCCTGATTCCTGAGAGGGGAGTGAAGGAGG 1860  
 Db 3016 GCTCTGCTTCTGTAACACTTCCCTGATTCCTGAGAGGGGAGTGAAGGAGG 3075  
 QY 1861 AAGAGGACAGCTGAGAGAGTGAAGCACAAGGGAGTGAAGGAGGAGCAGAGAGCAG 1920  
 Db 3076 AAGAGGACAGAGCTGAGAGAGTGAAGCACAAGGGAGTGAAGGAGGAGCAGAGAGCAG 3135  
 QY 1921 CAGAAAGTGGGTCTCTCAAGTCTCTCACTGAATCACTGAGACTCGAGAGCCGAGAGCCA 1980  
 Db 3136 CAGAAAGTGGGTCTCTCAAGTCTCTCACTGAATCACTGAGACTCGAGAGCCGAGAGCCA 3195  
 QY 1981 CAATGCTTCAGAAAGCTCAATGAACCCAGAGCCACATTTTCTTCCCTTAAGCATAGAC 2040  
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 QY 2041 AATGCAATTTGCAATTAACCAAAAAGATGACAGAGCTAATGAGTGGTGGCTTTGGCCTG 2100  
 Db 3256 AATGCAATTTGCAATTAACCAAAAAGATGACAGAGCTAATGAGTGGTGGCTTTGGCCTG 3315  
 QY 2101 GCAATTCAAAACTGGGACAGAGCAAGTGAATAATGACAGAGTGTGAATCTTTTCAACC 2160  
 Db 3316 GCAATTCAAAACTGGGACAGAGCAAGTGAATAATGACAGAGTGTGAATCTTTTCAACC 3375  
 QY 2161 TGACAGAGACCCCAAGCAGCTCAGAGAGTGAAGTGAAGCAGAGAGTGAAGCAGAGCC 2220  
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 QY 2581 TCAAGCTAGTCTTCTGCTGATTAATGATTTGGTTTTTGAAGAAATCAATTCAGCAGT 2640  
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 QY 2701 TTGTAAATGTCAGAGTCAAGCTTAAGCTTAAGTGAAGCAATCAATTAAGATTTCT 2760  
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 QY 2761 AGAGCAAACTGTGTTCTCACTGAGAGTGAAGTGAAGCAATTAAGTGAAGTGAAGT 2820  
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 QY 2941 ATTTGCTTTGTTTTTCTCTTTGGGTTTATTAATGAAGCAGAGATTTAATCTTAC 3000  
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 QY 3001 AGTCCAGAAAGCTGTGAATTTGAATGAAGAAAAATTAATTTTGTGTTTACACCTT 3060  
 Db 4216 AGTCCAGAAAGCTGTGAATTTGAATGAAGAAAAATTAATTTTGTGTTTACACCTT 4275  
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 QY 3121 ACAGTACCTGATTTTGTCAATTAACCAATTAAGATTAAGACATTTTATTAATTA 3180  
 Db 4336 ACAGTACCTGATTTTGTCAATTAACCAATTAAGATTAAGACATTTTATTAATTA 4395  
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 Db 4396 GTTGTGAGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 4455  
 QY 3241 TCCGCTGAGATCTGTTTTTAACAATTAATAAACAATTTAATTAATTTGAATTTGA 3300  
 Db 4456 TCCGCTGAGATCTGTTTTTAACAATTAATAAACAATTTAATTAATTTGAATTTGA 4515  
 QY 3301 TATATATTTTCAATTAATTTGTTTCTTTGTAATCTAATTTAATTAATTTGAAGAA 3360  
 Db 4516 TATATATTTTCAATTAATTTGTTTCTTTGTAATCTAATTTAATTAATTTGAAGAA 4575  
 QY 3361 TCTTTGAGAGAGTTCACAGATTTCAACATGAGGTTCTTGGCATGACACACAG 3420  
 Db 4576 TCTTTGAGAGAGTTCACAGATTTCAACATGAGGTTCTTGGCATGACACACAG 4635

QY 3421 AGTAAAGACTGATTTAGAGCTAAACATTCAGTGTGCTGAGATGCAAGACTGAATTT 3480  
 Db 4636 AGTAAAGACTGATTTAGAGCTAAACATTCAGTGTGCTGAGATGCAAGACTGAATTT 4695  
 QY 3481 AGAAAGTTCTCCCAAGATACACAGTGTGTTTAAAGCTAGGGGTGAGGGGGAAATCTGC 3540  
 Db 4696 AGAAAGTTCTCCCAAGATACACAGTGTGTTTAAAGCTAGGGGTGAGGGGGAAATCTGC 4755  
 QY 3541 CGCTTCATAGGAATGCTCCCTGGAGCTGGTAGGGGTGCTGCTGTTGTTGCTGCTG 3600  
 Db 4756 CGCTTCATAGGAATGCTCCCTGGAGCTGGTAGGGGTGCTGCTGTTGTTGCTGCTG 4815  
 QY 3601 GCTGTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660  
 Db 4816 GCTGTATTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4875  
 QY 3661 AGCATAGTCTGCGACAGTGCAGTGTCTCAATGAGTTTCAAGTGTGCAAGTGAATGAATATTA 3720  
 Db 4876 AGCATAGTCTGCGACAGTGCAGTGTCTCAATGAGTTTCAAGTGTGCAAGTGAATGAATATTA 4935  
 QY 3721 ACTAGAAATATATCTCTGTTGAAATCAGACACACAGTGTCTGCTGTTGAGTGTGTAC 3780  
 Db 4936 ACTAGAAATATATCTCTGTTGAAATCAGACACACAGTGTCTGCTGTTGAGTGTGTAC 4995  
 QY 3781 --GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3838  
 Db 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5055  
 QY 3839 GGGTATGGGTGCATTAATTTGGAGTGTCTTTTAAAGAACTCCAAACAGACTTCTGG 3898  
 Db 5056 GGGTATGGGTGCATTAATTTGGAGTGTCTTTTAAAGAACTCCAAACAGACTTCTGG 5115  
 QY 3899 AAGGTATTTTCTAAGAAATCTTGTGAGAGGTGAAGGCAACCCCTGTGACAGACCCC 3958  
 Db 5116 AAGGTATTTTCTAAGAAATCTTGTGAGAGGTGAAGGCAACCCCTGTGACAGACCCC 5175  
 QY 3959 ACCGAGCTCAAGTGGCCACTGTCTTCTCCCACTGAAGGGCTGCTCCCAATATTA 4018  
 Db 5176 ACCGAGCTCAAGTGGCCACTGTCTTCTCCCACTGAAGGGCTGCTCCCAATATTA 5235  
 QY 4019 TAAACCTCTGAGAGCTCAGGATGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 4078  
 Db 5236 TAAACCTCTGAGAGCTCAGGATGAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 5295  
 QY 4079 ACAGC 4083  
 Db 5296 ACAGC 5300

RESULT 7  
 US-10-244-633-2  
 ; Sequence 2, Application US/10244633  
 ; Publication No. US20030068640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nguyen, Thai D.  
 ; APPLICANT: Polansky, Jon R.  
 ; APPLICANT: Chen, Pu  
 ; APPLICANT: Chen, Hua  
 ; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,  
 ; TITLE OF INVENTION: Prognosis And Treatment Of Glioma And Related  
 ; FILE REFERENCE: 07425.0057.US01  
 ; CURRENT APPLICATION NUMBER: US/10/244,633  
 ; CURRENT FILING DATE: 2002-09-17  
 ; PRIOR APPLICATION NUMBER: US/09/306,828  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: US 09/227,881  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: Microsoft Word 97  
 ; SEQ ID NO 2  
 ; LENGTH: 5304  
 ; TYPE: DNA

; ORGANISM: Homo sapiens  
 US-10-244-633-2  
 Query Match 67.6%; Score 4057.4; DB 5; Length 5304;  
 Basic Local Similarity 99.7%; Pred. No. 0;  
 Matches 4077; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

QY 1 GCTCCACAGGAAGTCTCCCACTTGAACCTTGCATCAGATGTTACAGCCAGAACTC 60  
 Db 1216 GCTCCACAGGAAGTCTCCCACTTGAACCTTGCATCAGATGTTACAGCCAGAACTC 1275  
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 Db 1276 CGTGAAGGTGAAGGTCTGTGTCTTACACTGATATGCTTACACTGAGTCACTGC 1335  
 QY 121 AACCTGCTCCCAAGTTCAAGCAATTCCTGTGTCAAGCTCCCGAGTGGAGT 180  
 Db 1336 AACCTGCTCCCAAGTTCAAGCAATTCCTGTGTCAAGCTCCCGAGTGGAGT 1395  
 QY 181 ACAGGCGCAGCCCGGCTAAATTTTGTATTGTAGAGATGGAGTTTGCATATTAG 240  
 Db 1396 ACAGGCGCAGCCCGGCTAAATTTTGTATTGTAGAGATGGAGTTTGCATATTAG 1455  
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 Db 1456 CCGGCTGTCTTGAACCTCTGACCTCAAGTATCCACCACTCAGCTCTCTAAAGTC 1515  
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 Db 1516 TGGATTAACAGGCGATGAGTCAAGCGCCCGGCAAGGGGTGAGTTTAAATAGGAATTAAC 1575  
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 Db 1576 TTGAATGGTTACTTAAACCAACAGGGAACAGACAAAGCTGTGATATTTCAGGAGTTC 1635  
 QY 421 TTGGATGGGGAATGGTGCATGAGTGTCTGCTGATGCCAGACACTGCTCTATCA 480  
 Db 1636 TTGGATGGGGAATGGTGCATGAGTGTCTGCTGATGCCAGACACTGCTCTATCA 1695  
 QY 481 CTTTCTCCCTCATCCATTTTCAAGGCTAAGTTACATTTTATCACTGTTTGTG 540  
 Db 1696 CTTTCTCCCTCATCCATTTTCAAGGCTAAGTTACATTTTATCACTGTTTGTG 1755  
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 Db 1816 TCTGTGTGTGTATAGGGGAGAGGGCATACCCAGAGACTCCTTGAAGCCCGGAG 1875  
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 Db 1876 AGGTTTCTCCAGAGTGGGGAGGCGCTGCAAGCACCGGGGGTCTGGGGTGTCTGAGCA 1935  
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 Db 1936 ACCTGCAAGCCCGTGCACAGTGTGTTTGTATCACTCTGAGGACCTGTGTTCT 1995  
 QY 781 ATTCTGTGTGACTGTTCAATTCATCCAGGCAATTCATGAATTAATTAAGTACTTATA 840  
 Db 1996 ATTCTGTGTGACTGTTCAATTCATCCAGGCAATTCATGAATTAATTAAGTACTTATA 2055  
 QY 841 TCTGCAACACCCAGAGCAAAATGTGTAGCAAGGCACTGCGCTTACCTGCTGAG 900  
 Db 2056 TCTGCAACACCCAGAGCAAAATGTGTAGCAAGGCACTGCGCTTACCTGCTGAG 2115  
 QY 901 GTGACAGTTTCTCATGAAAGAGTGCAGAAAGAAATTAATGACCAACTTAACCA 960  
 Db 2116 GTGACAGTTTCTCATGAAAGAGTGCAGAAAGAAATTAATGACCAACTTAACCA 2175  
 QY 961 GTGCTAAAGAAAGAAATTAACACCATCTTGAAGAAATTTGCGAGCATCTCCTTAACAA 1020



Db 2176 GTGCTGAAGAAAGAAATTAACCACTTTGAAGAAATGTGCGCAGCATCCCTTAACA 2235  
QY 1021 GGCACCTCCCTAGCCGCCCTCTGCTGCTCATCTGTGCCGAGAGGCCGCCAAGCCGAGT 1080  
Db 2236 GGCACCTCCCTAGCCGCCCTCTGCTGCTCATCTGTGCCGAGAGGCCGCCAAGCCGAGT 2295  
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Db 2296 CTTTCAAGCTCTCTCTCATCATGTCACAGCGCTGACGTGCTGCTGCTGCTGCTGCTGCT 2355  
QY 1141 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db 2356 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2415  
QY 1201 AGAGGAAACTAGTCTAACTGAGAAATCTGAGAGGGAACAGTGTTCCTCAGAGGAAAAGG 1260  
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QY 1261 GCTTCCACGTCCAGAGAAATTCAGAGAGGTGGGAACCTGACAGGAGTGGGACCGTGGGAC 1320  
Db 2476 GCTTCCACGTCCAGAGAAATTCAGAGAGGTGGGACCTGACAGGAGTGGGACCGTGGGAC 2535  
QY 1321 TGAGCGGAGTCTGAAGAGGAGAAAGGTGAAAAGGCGAAGCTGACCTGCCAGATGTTT 1380  
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Db 4336 ACAGTACCTGTGATTTGTCTATTAACAATTAAGAAATCAACAGATTTTATTAATTAATTA 4395

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OY 3181 GTTGTGAGATAGCTGTGTAAGTAATATTATATCTCAAAACTACTTGTGAATTAAGACC 3240
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OY 3955 CCCCAACCCAGCTCAAGTGGCACTCTGTCTTCCCAATGAAGGCTGTGCTCCCAAGTA 4014
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Db 5176 CCCCAACCCAGCTCAAGTGGCACTCTGTCTTCCCAATGAAGGCTGTGCTCCCAAGTA 5235
OY 4015 TATATTAACCTCTCTGAGAGCTGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 4074
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OY 4075 CAGCAAGC 4083
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Db 5296 CAGCAAGC 5304

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RESULT 8  
US-10-244-633-34

; Sequence 34, Application US/10244633  
; Publication No. US20030068640A1

; GENERAL INFORMATION:

; APPLICANT: Nguyen, Thai D.

; APPLICANT: Polansky, Jon R.

; APPLICANT: Chen, Pu

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; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-34

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Query Match 66.9%; Score 4015.8; DB 5; Length 5271;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4051; Conservative 0; Mismatches 2; Indels 4; Gaps 3;

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OY 61 CGTAGAGGTGAGGGTCTGTGCTTACACCTACCTGATAGCTTACACCTGAGCTCACTGC 120
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Db 1276 CGTAGAGGTGAGGGTCTGTGCTTACACCTACCTGATAGCTTACACCTGAGCTCACTGC 1335
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Qy 901 GTGACAGTTTCTATGTGAAGACGTGCAAGAAATTTAATAGCCAGCACTTAAACCA 960  
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Db 2536 TGAGCGGAGTGTGAAGGAGGAGGAAAGGGGAGCTGCAAGCTCCAGAGTTC 2595  
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Qy 1801 GCTCTGTGTCTGTGAACAATTCCTGTGTATCTTCTGTGAGGGGAGTGTGAAGGG 1860  
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Qy 1921 CAGAACTGGGTGTCTCATCACTCTCTCATCTGATCACTGATCACTCAGAGCCGAGCCA 1980  
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Qy 2521 AGGGCAATCCGTTTCTTTTAAACAGAAAGAAACATTCCTAAGATTAAGCCAAACAGT 2580  
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[illegible]





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OY	3954	GCCCAACCCAGGCTCACTGTGGCCACCTCTGTCTTCCCATGAAGGGCTGGCTCCCACT	4013
Db	1740	GCCCCAACCAAGCTCACTGTGGCCACCTCTGTCTTCCCATGAAGGGCTGGCTCCCACT	1799
OY	4014	ATATATTAACCTCTCTGGAAGCTCAGGCAATGAAGCCAGCAAGCCATCCAGGACCTC	4073
Db	1800	ATATATTAACCTCTCTGGAAGCTCAGGCAATGAAGCCAGCAAGCCATCCAGGACCTC	1859
OY	4074	TCAGGACAGCAGAGGCTTTCAGAGGAACCTTCACCAACCTCTGCAATGAAGTTCTTCTG	4133
Db	1860	TCAGGACAGCAGAGGCTTTCAGAGGAACCTTCACCAACCTCTGCAATGAAGTTCTTCTG	1919
OY	4134	TGCAGTTGTCTCAGCTTGTGGGCTCGAAGATGCAGCTGTCCAGGCTGCTTCTGGCCTG	4193
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OY	4194	CCTGTGTGGGATGTGTGGGGGCCAGGACAGCTCAAGCTCAGAAAGGCATATGACAGATGG	4253
Db	1980	CCTGTGTGGGATGTGTGGGGGCCAGGACAGCTCAAGCTCAGAAAGGCATATGACAGATGG	2039
OY	4254	CCGAATCCAGATTAACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCAGAGCAGAG	4313
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OY	4314	CCAGGCAATGTCAAGTCAATCCATTACTTAACAGAGACAGGACGCCAACGCTTATGACT	4373
Db	2100	CCAGGCAATGTCAAGTCAATCCATTACTTAACAGAGACAGGACGCCAACGCTTATGACT	2159
OY	4374	GGAAGGCCAACAAGCTCGACTCAGCTCCCTGAGAGCCTCCTCCACCAATTGACCTTGGAA	4433
Db	2160	GGAAGGCCAACAAGCTCGACTCAGCTCCCTGAGAGCCTCCTCCACCAATTGACCTTGGAA	2219
OY	4434	CCAAGCTCCCAAGGCCCCAGAGAACCCAGAGAGGGCTGTGAGAGGAGCTGGCACTGTAG	4493
Db	2220	CCAAGCTCCCAAGGCCCCAGAGAACCCAGAGAGGGCTGTGAGAGGAGCTGGCACTGTAG	2279
OY	4494	GCGGAGGGGGAGCCAGGCTGGGAAACCCAAACAGAGAGTTGGAGCTGTCACAGCAACT	4553
Db	2280	GCGGAGGGGGAGCCAGGCTGGGAAACCCAAACAGAGAGTTGGAGCTGTCACAGCAACT	2339
OY	4554	CCTCCGAGACAAGTCAAGTTCTGAGAGGAAGAAAGCACTTAAGGCAAGAAATGAGAA	4613
Db	2340	CCTCCGAGACAAGTCAAGTTCTGAGAGGAAGAAAGCACTTAAGGCAAGAAATGAGAA	2399
OY	4614	TCGTGGCCAGAGGTTGGAAAGCAGACGCCAGAGAGTAGCAAGCTGGAAGAGGGCCAGTG	4673
Db	2400	TCGTGGCCAGAGGTTGGAAAGCAGACGCCAGAGAGTAGCAAGCTGGAAGAGGGCCAGTG	2459
OY	4674	TCCCCAATCCCGAACACTGCTGGGGCTGTGCCACAGGCTCCAGAGAGGTAAAGATGCG	4733
Db	2460	TCCCCAATCCCGAACACTGCTGGGGCTGTGCCACAGGCTCCAGAGAGGTAAAGATGCG	2519
OY	4734	AGAATGGGGGAGCTCTGAGTTCAACAGGTGATATGAGCTCCTGATAGCACTGCTACAGGCGC	4793
Db	2520	AGAATGGGGGAGCTCTGAGTTCAACAGGTGATATGAGCTCCTGATAGCACTGCTACAGGCGC	2579
OY	4794	TCCAGAGCCTCCCTGCTGCTGCTTCTCTTGAAGACTCAACAGCTAGCAACAAGACATGA	4853
Db	2580	TCCAGAGCCTCCCTGCTGCTGCTTCTCTTGAAGACTCAACAGCTAGCAACAAGACATGA	2639
OY	4854	ATTAAAGAAAGCAACAGGATCACTTCAAGTATTAAGTAATTAGCTCCTGAGACTT	4913
Db	2640	ATTAAAGAAAGCAACAGGATCACTTCAAGTATTAAGTAATTAGCTCCTGAGACTT	2699
OY	4914	CATTATTAATTAAGTATCAAGGTTCTTGTGGCCCTCCATATGACAGTTTTCACAGTCAATAG	4973
Db	2700	CATTATTAATTAAGTATCAAGGTTCTTGTGGCCCTCCATATGACAGTTTTCACAGTCAATAG	2759
OY	4974	CAAAAGGAAATTAAGAACCCGGGTAGATGTGTCATCAT	5014

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DB          2760  CAAAAGAGAAATATAAGACCGGCTAGATCTGTCTGCAT 2800
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RESULT 11
US-10-278-698-294
; Sequence 294, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: Patheonarray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-294

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Query Match	46.2%	Score 2773.4	DB 8	Length 2800
Best Local Similarity	99.9%	Pred. No. 0		
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Db 1 AGCCGAGGGGAGAGAGAAAG-AAAAGAGAGCGATGTGTATGAGCAAGAAAGACAGATTCAT				59
QY 2276 TCAAGGCGAGTGGGAATTGACCAAGGGAATTATAGTCACGATGATCTGGGTTCTAGAG				2335
Db 60 TCAAGGCGAGTGGGAATTGACCAAGGGAATTATAGTCACGATGATCTGGGTTCTAGAG				119
QY 2336 GCAGGCGTATNTGTGGGGGGAAAAATCAAGTTCAAGGAAAGTGGGAGACTGATATTC				2395
Db 120 GCAGGCGCTATATGTGTGGGGGGAAAAATCAAGTTCAAGGAAAGTGGGAGACTGATATTC				179
QY 2396 AATACATATTTTTCTTTTCAAGCTGAGTATTTCTGAGCAAGTCAGAGGTAATTAAGT				2455
Db 180 AATACATATTTTTCTTTTCAAGCTGAGTATTTCTGAGCAAGTCAGAGGTAATTAAGT				239
QY 2456 AGGCTGTAAATTAAGTATTAAGTTCTCCTTATTAAGAACTTTTCTCTGTGAGTTAGCA				2515
Db 240 AGGCTGTAAATTAAGTATTAAGTTCTCCTTATTAAGAACTTTTCTCTGTGAGTTAGCA				299
QY 2516 GCACAAAGGCAATCCGTTTCTTTTAAACAGAAAGAAAAATCTCTAAGAGTAAAGCCAA				2575
Db 300 GCACAAAGGCAATCCGTTTCTTTTAAACAGAAAGAAAAATCTCTAAGAGTAAAGCCAA				359
QY 2576 CAGATTCAACCTTAGTCTTGCTGCACTATATGATTTGGTTTTTGAATAATCATTTCAAGC				2635
Db 360 CAGATTCAACCTTAGTCTTGCTGCACTATATGATTTGGTTTTTGAATAATCATTTCAAGC				419
QY 2636 ATGTTTACTATCTGAATTCAGAAAATGAGACTAGAACCTTTGGCTGACCTGTAAACAACA				2695
Db 420 ATGTTTACTATCTGAATTCAGAAAATGAGACTAGAACCTTTGGCTGACCTGTAAACAACA				479
QY 2696 CCCATTGTAAATGTCTCAAGTTCAAGGCTTAACTGCAGAACCAATCAAAATTAAGATGAA				2755
Db 480 CCCATTGTAAATGTCTCAAGTTCAAGGCTTAACTGCAGAACCAATCAAAATTAAGATGAA				539
QY 2756 TCTTTAGAGCAACTGTGTCTTCACACTGTGAGGTGAGTCTGCAAGGCAAGTTTGAAA				2815
Db 540 TCTTTAGAGCAACTGTGTCTTCACACTGTGAGGTGAGTCTGCAAGGCAAGTTTGAAA				599
QY 2816 TATTTACTCACAAGATATGACACTGTGTGGTATTTAACAATAAAGTGTGCAAAAG				2875
Db 600 TATTTACTCACAAGATATGACACTGTGTGGTATTTAACAATAAAGTGTGCAAAAG				659
QY 2876 CAATCATATTTCAAGTGGCTTAAGTAACTTCTGACAGTTTGGTATATTTATGGCTA				2935

Db 660 CAATCATTAATTCAGAGTGGCTTAAAGTTACTCTGACAGTTTGGTATATTATATGGCTA 719  
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 Db 780 CCTACAGTCCAGAAAGCTGTGAATTTGAATGAGAAAAATACATTTTGTTTTACC 839  
 Oy 3056 ACCTTCTAATAATTTAATTTTATTTTCCATTGCGAATGAGCCATAACTCAAGTGG 3115  
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 Db 900 TAAATAAGTAACTGTGATTTTGTGATTAACCAATGAANAACACATTTTATCTATA 959  
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 Db 1020 AGACCTCTGCTGGAATCTTGTTTTACATATTAATAAAACATGTTTAAATTTGATAT 1079  
 Oy 3286 TTTGATTAATCAATTTTCAATATTTGTTTCTTGTGTAATCTAATTTTATATTTGA 3355  
 Db 1080 TTTGATTAATCAATTTTCAATATTTGTTTCTTGTGTAATCTAATTTTATATTTGA 1139  
 Oy 3356 AAAACATCTTCTGAGAAGAGTCCCGAGATTTCAACCAATGAGGTTCTTGAGACACACA 3415  
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 Oy 3416 CACAGATTAAGAACTGATTTAAGGCTAACATTTGACATTTGCTGAGATGCAAGACTG 3475  
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 Db 1260 AAATTAAGAAAGTTCTCCCAAAATACACAGTTGTTTAAAGCTAGGGGTGAAGGGGAAA 1319  
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 Db 1320 TCTGCGCTTCTATAGAAATGCTCTCCCTGAGACCTGTAAGGCTGCTCTTGTGTTCT 1379  
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 Db 1380 GGCCTGCTGTATTTTTCTCTGTCCCTGCTACGCTTAAAGGACTTGTGATCTCCAG 1439  
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 Db 1440 TTCCCTAGCATATGCTGTGACACAGTGCAGGTTCTCAATAGTTTGAAGTGAATGAAA 1499  
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 Db 1500 TATTAACCTAGAAATATATCTTGTGAATCAGACACCAAGTATCTGCTGTAAGTGG 1559  
 Oy 3776 TGTATC--GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3833  
 Db 1560 TGTATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1619  
 Oy 3834 TATTTGGGATATGGGTCATTAATTTGGGATGTTCTTTTAAAGAAATCTCCAAACGACT 3893  
 Db 1620 TATTTGGGATATGGGTCATTAATTTGGGATGTTCTTTTAAAGAAATCTCCAAACGACT 1679  
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 Db 1680 TCTGGAAGGTTATTTTCTAAGAACTTGTGCGAGGCTGAAGGCAACCCCTGTGTGACA 1739  
 Oy 3954 GCCCAGCCAGCTCACTGTGCACTGTCTTCCCGCATGAAGGCTGCTCCCACT 4013

Db 1740 GCCCAGCCAGCTCACTGTGCACTGTGTCTTCCCATGAAGGCTGCTCCCACT 1799  
 Oy 4014 ATATATAAACCCTCTGTGAGCTCAGGATGAGCCAGAAAGGCCACCATCCAGGACCTC 4073  
 Db 1800 ATATATAAACCCTCTGTGAGCTCAGGATGAGCCAGAAAGGCCACCATCCAGGACCTC 1859  
 Oy 4074 TCAGACAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTG 4133  
 Db 1860 TCAGACAGCAGAGCTTTCCAGAGAAAGCTCACCAAGCTCTGCAATGAGTTCTTCTG 1919  
 Oy 4134 TGCAGTTGCTGAGCTTTGGGCTGAGATGCGAGCTGTCCAGTGTGCTTCTGGGCTG 4193  
 Db 1920 TGCAGTTGCTGAGCTTTGGGCTGAGATGCGAGCTGTCCAGTGTGCTTCTGGGCTG 1979  
 Oy 4194 CCTGTGTGGGATGTGGGGGCGAGAGCAGCTCAGCTCAGAGAGGCAATGACAGAGTGG 4253  
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 Oy 4254 CCGATGCCAGTATACCTTCACTGTGTGCACTGCCAATGAATCCAGCTGCGCAGAGCAG 4313  
 Db 2040 CCGATGCCAGTATACCTTCACTGTGTGCACTGCCAATGAATCCAGCTGCGCAGAGCAG 2099  
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 Db 2100 CCAAGCCATGTCACTCATCTTCACTTACAGAGAGACAGCAGACCCCAAGCTTACACT 2159  
 Oy 4374 GAGAGCCACCAAGCTCAGCTCAGCTCCCTGAGAGGCTCTCCACCAATTTGACTTGA 4433  
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 Oy 4434 CCAAGCTGCGAGGCTCCCAAGAGACCCAGAGAGGCTGCAAGGAGACTGAGCACTGAG 4493  
 Db 2220 CCAAGCTGCGAGGCTCCCAAGAGACCCAGAGAGGCTGCAAGGAGACTGAGCACTGAG 2279  
 Oy 4494 GCGGAGGCGGAGCCAGCTGTGAACCCCAACCAAGAGTTGAGACTGTCTACAGAACCT 4553  
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 Db 2400 TCTGCGCAGAGGTTGAGAAAGCAGACGACAGAGGTAGCAAGGCTGAGAGGGCAGTG 2459  
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 Oy 4734 AGAGTGGGGGAGCTCTGAGTTCAAGCAGGTATATGAGCTGTAGTACCTGTACAGGCGC 4793  
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 Oy 4794 TCCAGGCTCTCCCTGCTGCTCCCTTCTCTAGAGCTGACAGCTAGCAAGACAGATGA 4853  
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 Oy 4854 ATTAAGAAAGCAGCAGCATCACTTCAAGTATCTAGTAAATTTAGTCTCTGAGAGCTT 4913  
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 Oy 4974 CAAAAGGAAATTAAGAGCCGGGTGAGATGTGTCTGCAT 5014  
 Db 2760 CAAAAGGAAATTAAGAGCCGGGTGAGATGTGTCTGCAT 2800

RESULT 12  
 US-10-278-698-808



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OY 4074 TCAGCAGCAGAGCTTTCAGAGAGAGCTCACCAGGCTCTGCAATGAGTTCTTCTG 4133
DB 1860 TCAGCAGCAGAGCTTTCAGAGAGAGCTCACCAGGCTCTGCAATGAGTTCTTCTG 1919
OY 4134 TGCAAGTTGCTGCAAGCTTTGAGGCTGAGATCCAGCTGTGCACTGCTTCTGAGCTG 4193
DB 1920 TGCAAGTTGCTGCAAGCTTTGAGGCTGAGATCCAGCTGTGCACTGCTTCTGAGCTG 1979
OY 4194 CTTGTTGAGATGTTGAGGCTGAGAGCAGCTCAGCTCAGAGAGAGGCAATGACAGAGTGG 4253
DB 1980 CTTGTTGAGATGTTGAGGCTGAGAGCAGCTCAGCTCAGAGAGAGGCAATGACAGAGTGG 2039
OY 4254 CCGATGCCAGTATACCTTCAAGTGTGGCCAGTCCCAATGATCCAGCTGCCAGAGCAGAG 4313
DB 2040 CCGATGCCAGTATACCTTCAAGTGTGGCCAGTCCCAATGATCCAGCTGCCAGAGCAGAG 2099
OY 4314 CCAAGGCTATGTCATTCATTAACCTTAACAGAGAGCAGAGCAGCAGCAGCAGCTTACCT 4373
DB 2100 CCAAGGCTATGTCATTCATTAACCTTAACAGAGAGCAGAGCAGCAGCAGCAGCTTACCT 2159
OY 4374 GGAAGGCCACCAAGGCTCAGCTCCCTGAGAGCCTCCCTCAACCAATTGACCTTGA 4433
DB 2160 GGAAGGCCACCAAGGCTCAGCTCCCTGAGAGCCTCCCTCAACCAATTGACCTTGA 2219
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DB 2400 TCTGACCAAGAGTTGAGAAAGCAGAGCAGAGAGTGAAGAGCTGAGAGAGGCGCAGT 2459
OY 4674 TCCCGAGACCGAGAGCACTGCTCGGAGCTGTCACCAAGGCTCCAGAGAGAGTGAAGT 4733
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DB 2700 CATTTAGATTAGTTGAGAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2759
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DB 2760 CAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2800
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RESULT 13
US-10-803-557-10
; Sequence 10, Application US/10803557
; Publication No. US20050095609A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
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; CURRENT APPLICATION NUMBER: US/10/803,557
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US/10/017,870
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-557-10

Query Match 46.2%; Score 2773.4; DB 9; Length 2800;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2797; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

OY 2216 AGCCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2275
DB 1 AGCCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 59
OY 2276 TCAAGGGCAGTGGGAATTTGACACAGGGATTAATAGTCCAGTGAATCCTGGTTCTAGAG 2335
DB 60 TCAAGGGCAGTGGGAATTTGACACAGGGATTAATAGTCCAGTGAATCCTGGTTCTAGAG 119
OY 2336 GCAAGGCTATATTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2395
DB 120 GCAAGGCTATATTGTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
OY 2396 AATCTATATTTTCTTTTACAGAGTGAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 2455
DB 180 AATCTATATTTTCTTTTACAGAGTGAATTTCTGAGAGAGAGAGAGAGAGAGAGAGAG 239
OY 2456 AGGCTGTAAGTTACTTATAGTTCTCTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2515
DB 240 AGGCTGTAAGTTACTTATAGTTCTCTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 239
OY 2516 GCACAAGGCAATCCCGTTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2575
DB 300 GCACAAGGCAATCCCGTTTCTTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
OY 2576 CAGATTCAAGCTTATGTTCTGCTGATATATGATTTGTTTGAAGAGAGAGAGAGAGAG 2635
DB 360 CAGATTCAAGCTTATGTTCTGCTGATATATGATTTGTTTGAAGAGAGAGAGAGAGAG 419
OY 2636 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2695
DB 420 ATGTTTACTATCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
OY 2696 CCCATTGTAAATGCTCAGAGTTCAAGGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 2755
DB 480 CCCATTGTAAATGCTCAGAGTTCAAGGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAG 539
OY 2756 TCTTTAGAGCAAACTGTGTTCTCCACTGAGAGTGTGCTGAGAGAGAGAGAGAGAGAG 2815
DB 540 TCTTTAGAGCAAACTGTGTTCTCCACTGAGAGTGTGCTGAGAGAGAGAGAGAGAGAG 599
OY 2816 TATTACTTCAAGATTTGACAGTGTGTTGATTAACAACATTAAGTGTCTCAAGAG 2875
DB 600 TATTACTTCAAGATTTGACAGTGTGTTGATTAACAACATTAAGTGTCTCAAGAG 659
OY 2876 CAATCATTAATTTCAAGTGGCTTAAAGTACTTCAAGAGTTTGGTATATTATTTGGCTA 2935
DB 660 CAATCATTAATTTCAAGTGGCTTAAAGTACTTCAAGAGTTTGGTATATTATTTGGCTA 719
OY 2936 TTGCAATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGTAAGAGAGAGATTAATTA 2995
DB 720 TTGCAATTTGCTTTTGTGTTTCTCTTGGGTTTATTAATGTAAGAGAGATTAATTA 779
OY 2996 CCTACAGTCCAGAAAGCCGTTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3055
DB 780 CCTACAGTCCAGAAAGCCGTTGAATTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
OY 3056 ACCTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3115
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QY 4014 ATATATTAACCTCTTGGAGCTCAGGATAGGACGAGAGCCACCCATCCAGGACCTC 4073
DB 1800 ATATATTAACCTCTTGGAGCTCAGGATAGGACGAGAGCCACCCATCCAGGACCTC 1859
QY 4074 TCAGCAGAGAGCTTTCAGAGAGAGCTTCAACAGCTTTCAGATAGAGTTCTTCTG 4133
DB 1860 TCAGCAGAGAGCTTTCAGAGAGAGCTTCAACAGCTTTCAGATAGAGTTCTTCTG 1919
QY 4134 TGCAGCTTGTGAGCTTTGGGCTGAGATGACAGCTGTCCAGCTGTGCTTGTGAGCTG 4193
DB 1920 TGCAGCTTGTGAGCTTTGGGCTGAGATGACAGCTGTCCAGCTGTGCTTGTGAGCTG 1979
QY 4194 CTTGTGTGGAGTGTGGGGCCAGAGACGCTCAGCTTCAAGAGGCCAATGACCAAGTGG 4253
DB 1980 CTTGTGTGGAGTGTGGGGCCAGAGACGCTCAGCTTCAAGAGGCCAATGACCAAGTGG 2039
QY 4254 CCGATGCCAGTATACCTTTCAGTGTGGGCACTCCCAATGAATCCAGCTGCCAGAGCAG 2099
DB 2040 CCGATGCCAGTATACCTTTCAGTGTGGGCACTCCCAATGAATCCAGCTGCCAGAGCAG 2099
QY 4314 CCAGGCAATGTCAATCATTCATTAACAGAGAGAGAGAGCCCAACGCTTAAAGCT 4373
DB 2100 CCAGGCAATGTCAATCATTCATTAACAGAGAGAGAGAGCCCAACGCTTAAAGCT 2159
QY 4374 GAGAGCCACCAAGCTCAGCTCAGCTCCCTGAGAGCTTCTCACCATTGAACCTTGA 4433
DB 2160 GAGAGCCACCAAGCTCAGCTCAGCTCCCTGAGAGCTTCTCACCATTGAACCTTGA 2219
QY 4434 CCAAGCTTCCAGGCTCCCAAGAGCCCAAGAGGGGCTGAGAGAGAGAGTGGGCACTTGA 4493
DB 2220 CCAAGCTTCCAGGCTCCCAAGAGCCCAAGAGGGGCTGAGAGAGAGAGTGGGCACTTGA 2279
QY 4494 GCGGAGCCGGGACCAAGCTGAGAAACCAAAACAGAGAGTGGAGAGCTGCCAGAGCAACCT 4553
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DB 2460 TCCCCAGACCCGAGACCTGCTGGGCTGAGCAACAGGCTCCAGAGAGAGTAAAGATGC 2519
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DB 2580 TCCAGGCTTCCCTGCTGCTGCTTCTCTAGAGAGCTGCAACAGTACCAAGACAGATGA 2639
QY 4854 ATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4913
DB 2640 ATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2699
QY 4914 CATTTAGATTAGTGTTCAGAGTTCCTGTGAGCTTCCATGTCAAGTTTTCAGAGTCCATAG 4973
DB 2700 CATTTAGATTAGTGTTCAGAGTTCCTGTGAGCTTCCATGTCAAGTTTTCAGAGTCCATAG 2759
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DB 2760 CAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2800

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RESULT 15  
 US-10-240-425-1586  
 ; Sequence 1586, Application US/10240425  
 ; Publication No. US2004003502A1

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; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT FILING DATE: US/10/240,425
; PRIOR FILING DATE: 2002-09-30
; PRIOR FILING DATE: PCT/US01/09847
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1586
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US2004003502A1 297171
US-10-240-425-1586

Query Match      17.8%; Score 1068.8; DB 7; Length 1086;
Best Local Similarity 99.6%; Pred. No. 46-251;
Matches 1082; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 3661 ACCATATGTCCTGGACAGTGTGAGTTCATATGATTTGAGAGTGAATATATA 3720
DB 1 ACCATATGTCCTGGACAGTGTGAGTTCATATGATTTGAGAGTGAATATATA 60
QY 3721 ACTAAGATATATCTCTTGTGAATCAGACACCAAGTCTGTGTATGATGTGTATC 3780
DB 61 ACTAAGATATATCTCTTGTGAATCAGACACCAAGTCTGTGTATGATGTGTATC 120
QY 3781 --GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3838
DB 121 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 3839 GGGTATGAGTGCATTAATTTGGATGTTCTTTTAAAGAACTCCAAAGACTTTGG 3898
DB 181 GGGTATGAGTGCATTAATTTGGATGTTCTTTTAAAGAACTCCAAAGACTTTGG 240
QY 3899 AAGTTATTTTCTAAGATCTTGTCTGAGAGCTGTGAAGGCAACCCCTGTGTGACAGCCCC 3958
DB 241 AAGTTATTTTCTAAGATCTTGTCTGAGAGCTGTGTGAAGGCAACCCCTGTGTGACAGCCCC 300
QY 3959 ACCGAGCTCAGAGTGGCACTCTGTCTTCCCTCCATGAAGGGCTGCTCCCATATATA 4018
DB 301 ACCGAGCTCAGAGTGGCACTCTGTCTTCCCTCCATGAAGGGCTGCTCCCATATATA 360
QY 4019 TAAACCTCTGAGAGCTCAGAGATGAGGACAGAGAGAGAGAGAGAGAGAGAGAGAG 4078
DB 361 TAAACCTCTGAGAGCTCAGAGATGAGGACAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 4079 ACAGAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4138
DB 421 ACAGAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 4139 GTTGTGAGAGCTTGGGGCTGAGAGTGCAGAGCTGTTCAGAGTGTCTTGTGAGCTGG 4198
DB 481 GTTGTGAGAGCTTGGGGCTGAGAGTGCAGAGCTGTTCAGAGTGTCTTGTGAGCTGG 540
QY 4199 TGTGGAGTGTGGGGCCAGAGACAGCTCAGCTCAGAGAGGCAATGACAGAGTGGCGAT 4258
DB 541 TGTGGAGTGTGGGGCCAGAGACAGCTCAGCTCAGAGAGGCAATGACAGAGTGGCGAT 600
QY 4259 GCCAGTATACCTTTCAGTGTGGCCAGTGTCCAAATGAAATCCAGTGTGCCAGAGAGCCAGG 4318
DB 601 GCCAGTATACCTTTCAGTGTGGCCAGTGTCCAAATGAAATCCAGTGTGCCAGAGAGCCAGG 660

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OY 4319 CCATGTCAGTCATCCATACTTAAGAGAGACAGCAGCACCCAACGCTTAGACCTGAGG 4378
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Db 661 CCATGTCAGTCATCCATACTTAAGAGAGACAGCAGCACCCAACGCTTAGACCTGAGG 720
    |||||
OY 4379 CCACCAAAAGTCGACTGAGCTCCCTGAGAGCTTCCTCCACCAATTGACCTTGACCAAG 4438
    |||||
Db 721 CCACCAAAAGTCGAGCTGAGCTCCCTGAGAGCTTCCTCCACCAATTGACCTTGACCAAG 780
    |||||
OY 4439 CTGCCAAGGCCCCAAGAGACCCAGAGAGGGCTGCAAGAGGAGCTGGGCACTCGAGGGGG 4498
    |||||
Db 781 CTGCCAAGGCCCCAAGAGACCCAGAGAGGGCTGCAAGAGGAGCTGGGCACTCGAGGGGG 840
    |||||
OY 4499 AGCGGACCAAGCTGGAACCCAAACCAAGAGATTGAGACTGCTACAGCAACTCTCTCC 4558
    |||||
Db 841 AGCGGACCAAGCTGGAACCCAAACCAAGAGATTGAGACTGCTACAGCAACTCTCTCC 900
    |||||
OY 4559 GAGACAAGTCAGTTCTGAGAGAAAGAAAGCACTAAGGCAAGAAAATGAAATCTGG 4618
    |||||
Db 901 GAGACAAGTCAGTTCTGAGAGAAAGAAAGCACTAAGGCAAGAAAATGAAATCTGG 960
    |||||
OY 4619 CCAGAGGTTGGAAGCAGCAGCCAGAGGTAGCAAGGCTGAGAAAGGGCCAGTGTCCCC 4678
    |||||
Db 961 CCAGAGGTTGGAAGCAGCAGCCAGAGGTAGCAAGGCTGAGAAAGGGCCAGTGTCCCC 1020
    |||||
OY 4679 AGACCCGAGACACTGCTGGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGACAGAT 4738
    |||||
Db 1021 AGACCCGAGACACTGCTGGGGCTGTGCCACAGGCTCCAGAGAAAGTAAAGATGACAGAT 1080
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OY 4739 GGGGGG 4744
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Db 1081 GGGGGG 1086
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Search completed: March 24, 2006, 07:53:22  
Job time : 4280 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2006, 02:07:22 ; Search time 1227 Seconds  
(without alignments)  
11401.984 Million cell updates/sec

Title: SEQ1-4037A

Perfect score: 6000  
Sequence: 1 gctccacaggaagtcctccccc.....atagggagagctttgttac 6000

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_NA\_New:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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- 11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631.6	10.5	632	US-09-925-065A-905501	Sequence 905501,
2	629.6	10.5	630	US-09-925-065A-917000	Sequence 917000,
3	570.6	9.5	571	US-09-925-065A-346049	Sequence 346049,
4	566.2	9.4	16525	US-11-136-527-717	Sequence 717, App
5	543	9.0	545	US-09-925-065A-346051	Sequence 346051,
6	541.4	9.0	545	US-09-925-065A-346050	Sequence 346050,
7	430.2	7.2	2068	US-11-136-527-2826	Sequence 2826, App
8	185.4	3.1	86361	US-10-995-561-13364	Sequence 13364, A
9	185.2	3.1	143389	US-11-112-908-30	Sequence 30, Appl
10	185.2	3.1	150314	US-11-112-908-24	Sequence 24, Appl
11	185.2	3.1	166020	US-11-112-908-28	Sequence 28, Appl
12	184.4	3.1	1744	US-11-072-512-1845	Sequence 1845, App
13	184	3.1	60754	US-10-995-561-13374	Sequence 13474, A
14	183.4	3.1	415117	US-10-995-561-13374	Sequence 13274, A
15	181.2	3.0	560	US-09-925-065A-137303	Sequence 127303,
16	180.6	3.0	1620	US-09-925-065A-67041	Sequence 67041, A
17	180.6	3.0	1620	US-09-925-065A-67042	Sequence 67042, A
18	180	3.0	2231	US-09-925-065A-703292	Sequence 703292,
19	179.8	3.0	491	US-09-925-065A-806860	Sequence 806860,
20	179.8	3.0	491	US-09-925-065A-806861	Sequence 806861,

21	179.6	3.0	14804	US-10-995-561-13379	Sequence 13379, A
22	179.6	3.0	98716	US-10-995-561-13331	Sequence 13331, A
23	179.6	3.0	191091	US-11-121-086-60	Sequence 60, Appl
24	179	3.0	159497	US-11-112-908-61	Sequence 61, Appl
25	179	3.0	171427	US-11-112-908-60	Sequence 60, Appl
26	178.8	3.0	506	US-09-925-065A-851208	Sequence 851208,
27	178.4	3.0	127917	US-10-775-169-82	Sequence 82, Appl
28	178.2	3.0	626	US-09-925-065A-655645	Sequence 655645,
29	178.2	3.0	626	US-09-925-065A-655646	Sequence 655646,
30	178.2	3.0	1056	US-09-925-065A-551984	Sequence 551984,
31	178.2	3.0	2675	US-09-925-065A-684565	Sequence 684565,
32	178	3.0	604	US-09-925-065A-949120	Sequence 949120,
33	178	3.0	624	US-09-925-065A-951830	Sequence 951830,
34	178	3.0	626	US-09-925-065A-949181	Sequence 949181,
35	177.8	3.0	615	US-09-925-065A-758120	Sequence 758120,
36	177.8	3.0	161994	US-11-112-908-57	Sequence 57, Appl
37	177.8	3.0	168656	US-11-112-908-59	Sequence 59, Appl
38	177.8	3.0	170285	US-11-112-908-58	Sequence 58, Appl
39	177.8	3.0	387780	US-10-995-561-13259	Sequence 13259, A
40	177.6	3.0	549	US-09-925-065A-860471	Sequence 860471,
41	177.6	3.0	549	US-09-925-065A-886633	Sequence 886633,
42	177.6	3.0	128978	US-10-775-169-345	Sequence 345, App
43	177.2	3.0	523	US-09-925-065A-163297	Sequence 163297,
44	177.2	3.0	549	US-09-925-065A-860470	Sequence 860470,
45	177	2.9	626	US-09-925-065A-655647	Sequence 655647,

## ALIGNMENTS

RESULT 1  
US-09-925-065A-905501  
Sequence 905501, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925, 065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243, 096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252, 147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250, 092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261, 766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289, 846  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FaastSeq for Windows Version 4.0  
SEQ ID NO 905501  
LENGTH: 632  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-905501  
Query Match 10.5%; Score 631.6; DB 6; Length 632;  
Best Local Similarity 99.8%; Pred No. 9.2e-05;  
Matches 611; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 69 TTAGGCTGTGTCTTACCTGATGCTTACACCTGAGCTCACTGACCTCTG 128  
DB 1 TTAGGCTGTGTCTTACCTGATGCTTACACCTGAGCTCACTGACCTCTG 60  
QY 129 CTTCCAGGTCACCAATTCCTCTGCTCAGCTCCCGGAGCTGAGGAGCGGC 188  
DB 61 CTTCCAGGTCACCAATTCCTCTGCTCAGCTCCCGGAGCTGAGGAGCGGC 120  
QY 189 ACGCCGCGATATTTTGTATGTTAGTAGAGATGGGTTTCAACATATTAGCCGCGCTG 248



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Db      121  AGCGCMGGCTAATTTTGTATTTGTAGTAGAGATGGGGTTTCACCATATTAAGCCGGCTG 180
Oy      249  GTCTTGAATCTCTGACCTCAGGTGATCCACCCTCAGGCTCTTAAAGTGCTGGATTA 308
Db      181  GTCTTGAATCTCTGACCTCAGGTGATCCACCCTCAGGCTCTTAAAGTGCTGGATTA 240
Oy      309  CAGGATGATGATCAGCGGCCCGGCCAAGGGTCAAGTGTATTAATGAAGAAATTAATTGAATGG 368
Db      241  CAGGATGATGATCAGCGGCCCGGCCAAGGGTCAAGTGTATTAATGAAGAAATTAATTGAATGG 300
Oy      369  TTTTACTAAACCAACGAGGAAACAGCAAAAGCTGTATTAATTTTCAAGGATTTCTTGGGATG 428
Db      301  TTTTACTAAACCAACGAGGAAACAGCAAAAGCTGTATTAATTTTCAAGGATTTCTTGGGATG 360
Oy      429  GGGAAATGGTCCATAGAGCTGCTGCTAGTCCAGACCACTGATCTCTATCATCTTTCTTC 488
Db      361  GGGAAATGGTCCATAGAGCTGCTGCTAGTCCAGACCACTGATCTCTATCATCTTTCTTC 420
Oy      489  CCTCATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAAGCT 548
Db      421  CCTCATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAAGCT 480
Oy      549  CCACATCGTTACTGAATAATGAATATACATAAAGTATTTCCATTTGGGGCCATCTGTGTG 608
Db      481  CCACATCGTTACTGAATAATGAATATACATAAAGTATTTCCATTTGGGGCCATCTGTGTG 540
Oy      609  TGTGTATAGGGAGAGGAGGATACCCCAAGAGACTCTTGAAGCCCCCGGACAGAGGTTTCC 668
Db      541  TGTGTATAGGGAGAGGAGGATACCCCAAGAGACTCTTGAAGCCCCCGGACAGAGGTTTCC 600
Oy      669  TCTCCAGCTGGGGAGACCTCTGCAAGACCCGG 700
Db      601  TCTCCAGCTGGGGAGACCTCTGCAAGACCCGG 632

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RESULT 2
US-09-925-065A-917000/c
/ Sequence 917000, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 917000
/ LENGTH: 630
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-917000

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Query Match      10.5%; Score 629.6; DB 6; Length 630;
Best Local Similarity 99.8%; Pred. No. 0.0001;
Matches 629; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy      70  GAGGCTCTGTGCTTACACCTACCTGATAGCTTACACCTGAGGCTCATGCAACCTCTGC 129
Db      630  GAGGCTCTGTGCTTACACCTACCTGATAGCTTACACCTGAGGCTCATGCAACCTCTGC 571
Oy      130  CTCACAGTTCAAGCAATTCCTCTGTCTCAGGCTCCCGGTAGCTGGACTACAGGCGCA 189

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Db      570  CTCCAGGTTCAACCAATTCCTCTGTCTCAGGCTCCCGGATGAGCTGGAGACTACAGCGCA 511
Oy      190  GCGCGGCTAATTTTGTATTTGTAGTAGAGATGGGGTTTACACCATATTAAGCCGGCTGG 249
Db      510  GCGCGGCTAATTTTGTATTTGTAGTAGAGATGGGGTTTACACCATATTAAGCCGGCTGG 451
Oy      250  TCTTGAATCTCTGACCTCAGGTGATCCACCCTCAGGCTCTTAAAGTGCTGGATTAAC 309
Db      450  TCTTGAATCTCTGACCTCAGGTGATCCACCCTCAGGCTCTTAAAGTGCTGGATTAAC 391
Oy      310  AGGATGATGATCAGCGGCCCGGCCAAGGGTCAAGTGTATTAATGAAGAAATTAATTGAATGG 369
Db      390  AGGATGATGATCAGCGGCCCGGCCAAGGGTCAAGTGTATTAATGAAGAAATTAATTGAATGG 331
Oy      370  TTACTAAACCAACGAGGAAACAGCAAAAGCTGTATTAATTTTCAAGGATTTCTTGGGATGG 429
Db      330  TTACTAAACCAACGAGGAAACAGCAAAAGCTGTATTAATTTTCAAGGATTTCTTGGGATGG 271
Oy      430  GGAATGGTCCATAGAGCTGCTGCTAGTCCAGACCACTGATCTCTATCATCTTTCTTC 489
Db      270  GGAATGGTCCATAGAGCTGCTGCTAGTCCAGACCACTGATCTCTATCATCTTTCTTC 211
Oy      490  CTCAATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAAGCTTC 549
Db      210  CTCAATCTCTCATTTTCAAGGCTAAGTTACCATTTTATTCACCAATGCTTTTGTGTAAAGCTTC 151
Oy      550  CACATCGTTACTGAATAATGAATATACATAAAGTATTTCCATTTGGGGCCATCTGTGTG 609
Db      150  CACATCGTTACTGAATAATGAATATACATAAAGTATTTCCATTTGGGGCCATCTGTGTG 91
Oy      610  GTGTATAGGGAGAGGAGGATACCCCAAGAGACTCTTGAAGCCCCCGGACAGAGGTTTCT 669
Db      90  GTGTATAGGGAGAGGAGGATACCCCAAGAGACTCTTGAAGCCCCCGGACAGAGGTTTCT 31
Oy      670  CTCACAGCTGGGGAGACCTCTGCAAGACCCGG 699
Db      30  CTCACAGCTGGGGAGACCTCTGCAAGACCCGG 1

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RESULT 3
US-09-925-065A-346049
/ Sequence 346049, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 346049
/ LENGTH: 571
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-346049

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Query Match      9.5%; Score 570.6; DB 6; Length 571;
Best Local Similarity 99.8%; Pred. No. 0.0011;
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2672 CCTTGGTCAGCTGTAACAAACCCATTGTAATGTCGAAGTCAGGCTTAACCTGC 2731  
 DB 1 CCTTGGTCAGCTGTAACAAACCCATTGTAATGTCGAAGTCAGGCTTAACCTGC 60  
 QY 2732 AGAACCAATGAATTAAGATAGATCTTTAGAGAACTGTGTTCTCCACTGCGAGGT 2791  
 DB 61 AGAACCAATGAATTAAGATAGATCTTTAGAGAACTGTGTTCTCCACTGCGAGGT 120  
 QY 2792 GAGCTGCGCAGGCGAGTTGGAAATATTTACTTCAAGATTTGACACTGTGTGGTAT 2851  
 DB 121 GAGCTGCGCAGGCGAGTTGGAAATATTTACTTCAAGATTTGACACTGTGTGGTAT 180  
 QY 2852 TAAACAATTAAGTTGCTCAAGGCAATCAATTTCAAGTGGCTTAAGTACTTGA 2911  
 DB 181 TAAACAATTAAGTTGCTCAAGGCAATCAATTTCAAGTGGCTTAAGTACTTGA 240  
 QY 2912 CAGTTTGTATATTTATGCGTATGCGCATTTGCTTTTGTCTTCTTGGGTTTA 2971  
 DB 241 CAGTTTGTATATTTATGCGTATGCGCATTTGCTTTTGTCTTCTTGGGTTTA 300  
 QY 2972 TTAATGAAAGCAGGATTTATTAACCTACAGTCAGAAAGCCTGTGAATTTGAATGAGA 3031  
 DB 301 TTAATGAAAGCAGGATTTATTAACCTACAGTCAGAAAGCCTGTGAATTTGAATGAGA 360  
 QY 3032 AAAAATTAATTTTGTGTTTACCACTTCTAACTAATTTAACTTTTATTCATTCG 3091  
 DB 361 AAAAATTAATTTTGTGTTTACCACTTCTAACTAATTTAACTTTTATTCATTCG 420  
 QY 3092 AATAGAGCCATAAATCTCAAGTGTATTAACAGTACCTGTGATTTTGTCTTACCAATG 3151  
 DB 421 AATAGAGCCATAAATCTCAAGTGTATTAACAGTACCTGTGATTTTGTCTTACCAATG 480  
 QY 3152 AATACACAGCATTTTATCTATATTAACAGTGTGAGATAGCTTGAATGAATATT 3211  
 DB 481 AATACACAGCATTTTATCTATATTAACAGTGTGAGATAGCTTGAATGAATATT 540  
 QY 3212 TATACTCAAAACTCTTTGAATTAAGACCTC 3242  
 DB 541 TATACTCAAAACTCTTTGAATTAAGACCTC 571

RESULT 4  
 US-11-136-527-717  
 ; Sequence 717, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Nouns, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO 717  
 ; LENGTH: 16525  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-11-136-527-717

Query Match 9.4%; Score 566.2; DB 12; Length 16525;  
 Best Local Similarity 62.6%; Pred. No. 0.0001;  
 Matches 1201; Conservative 0; Mismatches 608; Indels 110; Gaps 16;  
 QY 3164 TTTTATATTAATTAAGTTGTGAGATAGCTGTGAATGAATTTATTAATCAAAAC 3223  
 DB 5339 TTTATATCCGTGTATAGCTGATGAGCTTTCATGAAA---TGTGTATGTAATCAAGG 5395  
 QY 3224 TACTTTGAATTAAGACTCTGCTGATCTGTTTAAATTAATTAATTAATCAATGTTTA 3283  
 DB 5396 TCTTTAAATTAAGACTTGAATGCTGATCTTATTAATTAATTAATTAATCAAGGTTTAA 5455

QY 3284 AATTTGATATTTTATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3343  
 DB 5456 TATTTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5503  
 QY 3344 TATATATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3403  
 DB 5504 TATATATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5562  
 QY 3404 GGCATGACACACAGAGTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3463  
 DB 5563 GGCATGACACACAGAGTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5611  
 QY 3464 GATGCAAGCTGAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3523  
 DB 5612 GATGCAAGCTGAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5671  
 QY 3524 TGAAGGGGGAATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3583  
 DB 5672 GGGCGGCATCATGTTTCTCAACCT-----TGTGTGGAGCTTAAGGCTGTGG 5719  
 QY 3584 TCTTGTGTTCTGCTGCTGCTGTTATTTTCTGTCCTGCTACGCTTAAAGACTGTG 3643  
 DB 5720 GCACTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5778  
 QY 3644 TTGAATCTGAGTTCTTACATAGTCCGACAGTGAAGTGTTCATAGACTTTCAG 3703  
 DB 5779 CTGTCTCTTATGTTCTTACATAGTCCGACAGTGAAGTGTTCATAGACTTTCAG 5826  
 QY 3704 AGTGAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3762  
 DB 5827 -----TGAACACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5879  
 QY 3763 TGTGTATGTTGTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3822  
 DB 5880 CAGACAGGTGGACATACGCGGACATGT-----ACAAACAGGCTTGAAGAAC 5924  
 QY 3822 ATAGGAACATTAATTTGGGGTATGGGGTATGGGGTATGGGGTATGGGGTATGGGGTATGGGG 3882  
 DB 5925 TTAGGGGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5981  
 QY 3883 CCAAAACAGACTTCTGAAGTATTTTCTAAGATCTTGTGCTGAGCGTGAAGCAACC 3942  
 DB 5982 AAAATAGCTCTGGGGCTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 6041  
 QY 3943 CCTGTGAC-----AGCCCAACCAAGCTTCAAGTGGCCAGCTGTGTCTTCCCAT 3994  
 DB 6042 TCTATATCCCCCATGAGTGTGTCACACCAAGCTTCAAGTGGCCAGCTGTGTCTTCCCAT 6101  
 QY 3995 GAAAGGCTGCTGCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4054  
 DB 6102 AAGAGGCTGCTGCCCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6161  
 QY 4055 CCAACCATCAAGGCACTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 4114  
 DB 6162 CCAACCATCAAGGCACTCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 6216  
 QY 4115 CTGCAATAGGTTCTTCTGTGACGTTGCTGAGCTTGTGGCTGAGATGCAAGTGTTC 4174  
 DB 6217 TCATACCAATGCTCTCTGTGACGTTGCTGAGCTTGTGGCTGAGATGCAAGTGTTC 6276  
 QY 4175 AGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4234  
 DB 6277 AGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6336  
 QY 4235 AGGCCAATGACCAAGTGGCGATGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4294  
 DB 6337 AGGCCAATGACCAAGTGGCGATGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6396  
 QY 4295 CCAAGTCTCCAGAGCAGAGCCAGCTATGATGATCAATTAATTAATTAATTAATTAATTAATTAAT 4354  
 DB 6397 CTAAGTCTCCAGAGCAGAGCCAGCTATGATGATCAATTAATTAATTAATTAATTAATTAATTAAT 6456

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OY 4355 GCACCCAACTGTTAGCTGAGGCGCAACAAAGCTCGACTGCTCCTGAGAGAGCTCC 4414
    |||
Db 6457 GCATTCAGCATGACGACTAGATGTCACCAAGGCCGGGTGAGATCCTTGAGAGTCTCC 6516
OY 4415 TCACCAATTGACTTGGACCAAGGCTGACAGCCCTCAGAGAACCCAGAGAGGGCTGCAGA 4474
    |||
Db 6517 TCACCAAGATACCTCAGAGCGAGAGTACTGAGACCCAGAGAGGTCCAGAGAGGGCTACAG 6576
OY 4475 GGGAGCTGGGACCCCTGAGGCGGAGCGGAGCAAGCTGAAACCAACCAAGAGGTGG 4534
    |||
Db 6577 GCGAGCTGGGTGCTGCTGAGAGAGAGCGGAGCAAGCTGAGAACCAACCAAGAGTCTGG 6636
OY 4535 AGACTGCTTACAGCAACCTCTCCGAGACAAATGCTGTTGAGAGAGAGAGAGAGCAG 4594
    |||
Db 6637 AGGTAGCTTATTAACATCTCTGAGAGACAAATGAGTCTTGGAGAGAGAGAGAGCAGC 6696
OY 4595 TAAAGCAAGAAATGAGAAATCTGCGCAGAGAGTTGAAAGCAGCAGCAGAGAGTACGA 4654
    |||
Db 6697 TGGAACAAAGAAATTAAGATTTGGCCAGAGAGCTAGAGAGCAGCAGAGAGTACGA 6756
OY 4655 GGGTGAAGAGGGGCGAGTGTCCCGAGACCCGAGACATGCTCGGGCTGTGCGACAGGCT 4714
    |||
Db 6757 GGGTGAAGAGAGCGAGTGTCTCTACCCACACCCCTCTGAGACATGTTGCCAGGCT 6816
OY 4715 CCAGAGAAAGTAAAGATCAGAGTGGGGGAGCTCTGAG-TCAGCAGGTGATATGCTCG 4773
    |||
Db 6817 CCAGAGAAAGTAAAGATCAGAGTGGGGGAGCTGAGTACCCGAGAGTACAGTTCG 6876
OY 4774 TAGTACTGCTACAGCGGCTCCAGGCTCCTGCTGCTGCTTTT-----CTAGAGA 4827
    |||
Db 6877 GGGTGACCTATTAACAGAGCTCCAGGCTTCTCTTTTGTGCTTTTCTCAGTAAA 6936
OY 4828 CTGCAAGCTAGCAACAAGATGAATTAAGAAAGACAGCAGATCACTTCAAGTAT 4887
    |||
Db 6937 CTGAAAGTCCAGTATGAGTATGCTTCAATTAAGAAAGAGCAACCTTTTATGTT 6996
OY 4888 ACTAGTAATTTAGCTCTGAGAGCTTCAATTAAGTATGTTGAGTCTTGTGCCCC 4947
    |||
Db 6997 TCTGCAAGTTGACT-----CGTTGTTAGGCAAGTGAATCTGTAATCTGCTCA 7048
OY 4948 TCCATGTCAGTTTTCACAGTCCATGCAAAAGAGAGAAATTAAGAGACCGGTTGAGATGTG 5007
    |||
Db 7049 GTCAAGACAAATGATCAACAGCAGCAGCAAGCAATGAGAAACACGGGGCCCAAGGAGAGG-- 7106
OY 5008 TCTGATATGAGCAGTAAAGAGTTGCAATGTCCTTTTGAAGAACTATCTTTTGG 5066
    |||
Db 7107 --TGCAATGTGAATAGAAATGGCTGTGCTGCTTGGGTCAATTTTCAAGCTTGG 7163
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RESULT 5  
US-09-925-065A-346051

/ Sequence 346051, Application US/09925065A  
/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ CURRENT FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 346051

/ LENGTH: 545  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-09-925-065A-346051

Query Match 9.04; Score 543; DB 6; Length 545;  
Best Local Similarity 99.6%; Pred. No. 0.0034;  
Matches 543; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 3648 ATCTCAGTTCCTGATAGGCTGAGCAGAGTGCAGAGTTCCTCAATGATTTGAGAGTG 3707
    |||
Db 1 ATCTCAGTTCCTGATAGGCTGAGCAGAGTTCCTCAATGATTTGAGAGTG 60
OY 3708 AATGAAATATTAACCTAAGAAATATATCTTGTGAAATCAGACACCAAGTATGCTG 3767
    |||
Db 61 AATGAAATATTAACCTAAGAAATATATCTTGTGAAATCAGACACCAAGTATGCTG 120
OY 3768 TAAGTGTGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3827
    |||
Db 121 TAAGTGTGTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
OY 3828 AACTATTATGGGGTATGGGTGCAATAATTGGAGTGTCTTTTAAAGAACTCCAAA 3887
    |||
Db 181 AACTATTATGGGGTATGGGTGCAATAATTGGAGTGTCTTTTAAAGAACTCCAAA 240
OY 3888 CAGACTTCTGAGAGTATTTTCTAAGATCTTGTGCGAGCGTGAAGCAACCCCTG 3947
    |||
Db 241 CAGACTTCTGAGAGTATTTTCTAAGATCTTGTGCGAGCGTGAAGCAACCCCTG 300
OY 3948 TGCAAGCCCAACCCAGCTCAGGTGACCTCTGTCTTCCCGCATGAAGGGCTGCTC 4007
    |||
Db 301 TGCAAGCCCAACCCAGCTCAGGTGACCTCTGTCTTCCCGCATGAAGGGCTGCTC 360
OY 4008 CCCAGTATATTAACCTCTGAGGCTCAGGAGTGAAGCCAGAGGCAACCCATCCAG 4067
    |||
Db 361 CCCAGTATATTAACCTCTGAGGCTCAGGAGTGAAGCCAGAGGCAACCCATCCAG 420
OY 4068 CACCTTCAGCAGCAGAGCTTTCAGAGAGAGCTTCAACCAAGCTCTGCAATGAGTT 4127
    |||
Db 421 CACCTTCAGCAGCAGAGCTTTCAGAGAGAGCTTCAACCAAGCTCTGCAATGAGTT 480
OY 4128 CTTCTGTCAGCTGCTGAGCTTTGGGCTTGAATGTCAGAGTCCAGTGTCTTCT 4187
    |||
Db 481 CTTCTGTCAGCTGCTGAGCTTTGGGCTTGAATGTCAGAGTCCAGTGTCTTCT 540
OY 4188 GGCCCT 4192
    |||
Db 541 GGCCCT 545
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RESULT 6

US-09-925-065A-346050

/ Sequence 346050, Application US/09925065A

/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ CURRENT FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 346050
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-346050

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Query Match	9.0%;	Score 541.4;	DB 6;	Length 545;
Best Local Similarity	99.4%;	Pred. No. 0.0037;		
Matches 542;	Conservative	1;	Mismatches	2; Indels 0

[illegible]

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RESULT 7
US-11-136-527-2826
: Sequence 2826, Application US/11136527
: Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
: TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
: FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
: PRIOR FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2826
LENGTH: 2068
: TYPE: DNA
: ORGANISM: Rattus norvegicus
US-11-136-527-2826

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Query Match 7.2%; Score 430.2; DB 12; Length 2068;

Best Local Similarity 77.4%; Pred. No. 0.11;  
Matches 527; Conservative 6; Mismatches 144; Indels 4; Gaps 1.

OY	4043	GAGCAGCAAGGACACCCATCCAGGACCTCTCAGCAGCAGAGAGCTTTCAGAGGAAGC	4102
Db	2	GAGGAGCAAGGGCCACCATCCAGACACTTTCAGCAGAGC-----CTTCTAGAAATGATAGC	57
OY	4103	CTCACCAAGCCTCTGCATATGAGGTTCTTCTGTGACGTTGCTGACGTTTGGGCGTGA	4162
Db	58	CTCACCCAGCCCTTCAATCCGATGCGCTCTCTGTGACATCTGTCGAGCTCGGTCCCAAGA	117
OY	4163	TGCGAGCTGTCCAGCTGCTGCTTCTTGCGCTGCGCTGGTGTGGAGTGTGGGGGCCAGGACAG	4222
Db	118	TGCCAGCTCTCCAGCTGCTGTTTCTTGCGCTGCGCTGGTGTGGAGTGTGGGGGCCAGGACAG	177
OY	4223	CTCAGCTCAGAAAGGCCAATGATGACCAAGATGGCCGATGCGCATATATCTTTCAGTGTGCCA	4282
Db	178	CACAGTTCGAAAGGCCCAACGATCGAGATGGTTCATGTCGACAGTACACCTTCACTGTGGCCA	237
OY	4283	GTCCCAATGATTCAGCTGCGCCAGAGAGAGCCAGGCGCATATGTCATATCCATATCTTAC	4342
Db	238	GCCCAATGAAATCTAGCTGCGCCAGAGAGAGACAGGCCCATGTCAAGCATTCAGACCTTTC	297
OY	4343	AGAGAGACAGCAGCACCCACGTTTAGACCTGAGGCGCACCAAACTGCACTCAGCTGCC	4402
Db	298	AGAGAGATAGCAGCATCCAGATGCAGACCTAGAGTCCACCAAGCCCGGTCAGATGCC	357
OY	4403	TGAGAGGCTTCTTCCACCAATTGAACCTTTGGAACCAAGCTGCCAGGCCCCAGAGACCCAG	4462
Db	358	TGAGAGATCTCTCCACACAGATGACCTTCAGGCGGAGTTATCTGGGAGCCAGAGGCTCCAGG	417
OY	4463	AGGGGCTGCAGAGGAGGCTGGGCAACCTGAGAGCGGAGCGGAGACAGCTGGAAACCCAA	4522
Db	418	AGGGGCTTACAAAGGCGCACCTGGGTGCCCTTGAGAGAGAGACGGGACACACTGAGACSCAA	477
OY	4523	CCAGAGATTTGAGACTGCTTACAGCAACTCTCTCGAGACAACTCAATCTCTGAGGAG	4582
Db	478	CCAGGAGATCTGAGAGTAGCTTATTAACAATCTCTGAGAGACAAATCAGCTTTGGAGGAG	537
OY	4583	AGAGAAAGCGACTTAAGGCGCAAGAAAATGAAATCTGGCGAGAGGTTGGAAAGCAGCAGCC	4642
Db	538	AGAAAGAGCAGCTTGAAACAGAGAAATTAAGATTTGGCGAGAGGCTTGAAGGCGCAGCGCC	597
OY	4643	AGAGAGTACAGAGCTGAGAAAGGGGCCAGTGTCCCGACAGACCCGAGACACTGCTCGGCTG	4702
Db	598	AGAGAGTACAGAGGCTGAGAGAGGGCCAGTGTCTTCAACCCACACACCCTCTCAGAGCA	657
OY	4703	TGCCACACAGGCTCCAGAGGAG 4723	
Db	658	TGTTTCCAGGCTCCAGAGGAG 678	

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RESULT 8
US-10-995-561-13364/C
: Sequence 13364, Application US/10995561
: Publication No. US2005027054A1
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
: TITLE OF INVENTION: DETECTION AND USES THEREOF
: FILE REFERENCE: C1001559
: CURRENT APPLICATION NUMBER: US/10/995,561
: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ ID NOS: 85702
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13364
: LENGTH: 86361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(86361)

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PRIOR FILING DATE: 2004-04-23





